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Result
No.
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-MODEL-frame+ p2n.model -DEV=xlh
-MODEL-frame+ p2n.model -DEV=xlh
-Q-/cgn2 1/USPTO_spool/US09651651/runat_18112005_101830_20245/app_query.fasta_1.711
-DB=GenEmb1 -QFMT-fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTPMT=pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER-US09651651_@CGN 1 1 3367 @runat 18112005 101830 20245 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBICOK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THEBADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THEBADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                           Query
Score Match Length DB ID
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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1: gb_ba:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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ALIGNMENTS

Alignment Scores: Pred. No.: Score:	ORIGIN				SECTIONS	JOURNAL	TITLE	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	AX090311	RESULT 1
cores: 5.65e-246 2965.00	ı	/mol_type /db xref=			Location Joration	MONGANTO COMPANY (IIS)	Plant sterol acyltransterases	Lassner, M. and van Eenennaam, A.	יי	Spermatophyta; Magnollophyta; eudicotyledons; cole educotyledons rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Iracheophyta;	Arabidopsis thaliana	Arabidopsis thaliana (thale cress)	•	AX090311.1 GI:13444180	AX090311	Sequence 4 from Patent WO0116308.	AX090311		
-246 Length:)0 Matches:		/mol_type="unassigned DNA" /db xref="taxon:3702"	organism="Arabidopsis thaliana"	,	Location/Qualifiers	(III)	ransterases	Eenennaam, A.		I; Brassicales;	lantae; Streptop	ina	na (thale cress)		44180		tent W00116308.	1641 bp		
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mRNA, partial cds.
AY989885
AY989885.1 GI:6627190
                        Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1899)
Banas,A., Carlsson,A.S., Huang,B., Lenman,M., Banas,W., Lee,M.,
Noiriel,A., Benveniste,P., Schaller,H., Bouvier-Nave,P. and
Stymne,S.
                     Agricultural Sciences,
Sweden
                                                                                                                                                  Arabidopsis thaliana synthesizes sterol esters related to the animal lecithin: cholesterol acy
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AY989885
                                                                                                                              Unpublished
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phospholipid:sterol acyl transferase (PSAT)
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acyltransferase
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PLN 01-JUN-2005

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420 1200 400 1140

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ProThrLysLeuGluGluArgAspLeuTyrPheHisLysLeuLysLeuThrPheGluThr 180
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                                                                                      GATCCAGGTTACATAACAGGTCCTCTTTCTACTGTCTGGAAAGAGTGGCTTAAGTGGTGT
                                                                                                   AspProGlyTyrIleThrGlyProLeuSerThrValTrpLysGluTrpLeuLysTrpCys
                                                                                                                                      ACAGACCATCCCGAGTGTAAGTCACGGCCTGACAGTGGTCTTTCAGCCATCACAGAATTG
                                     GTTGAGTTTGGTGTAGAAGCAAATGCAATTGTCGCTGTTCCATACGATTGGAGATTGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  phospholipids to sterols"
/codon_start=1
/codon_start=1
/protein_id="phospholipid:sterol acyl transferase"
/protein_id="AAY43920.1"
/protein_id="AAY43920.1"
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SKNCKGUNTFWTHFSGGAAKKDKAVYHCDEEEYQSKYSGMPTNIINIEISTSVTETA
LVNMTSNECGLFTLLSFTARELADGTLFKAIEDYDPDSKRMLHQLKTHDDPVFNPL
TPWERP PPIKNVFCIYGAHLKTEVGYYFAPSGKPYPDNWIITDIIYETEGSLVSRSGTV
VDGNAGETTGDETYPYHSLSWCKNWLGFSKVNITWAFQPEHDGSDWHLENUTHEHGSD
IIANMTKAPRVKYITFYEDSESIPGKRTAVWELDKTNHRNIVRSPVLMRELMLQMWHD
IQPGAKSKFVTKAKRGPLRDADCYWDYGKACCAWQBYCEYRYSFGDVHLGQSCRLRNT
GANMT.OTYT"
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   GlySerLeuValSerArgSerGlyThrValValAspGlyAsnAlaGlyProIleThrGly
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                                                                ValAspHisGluHisGlySerAspIleIleAlaAsnMetThrLysAlaProArgValLys
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                                                                                                                                                    GATGAGACGGTACCCTATCATTCACTCTCTTGGTGCAAGAATTGGCTCGGACCTAAAGTT
                                                                                                                                                                 AspGluThrValProTyrHisSerLeuSerTrpCysLysAsnTrpLeuGlyProLysVal
                                                                                                                                                                                                                                                     CCAAGTGGCAAACCTTATCCTGATAATTGGATCATCACGGATATCATTTATGAAACTGAA
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                                                                                                    AACATAACAATGGCTCCCCAGCCAGAACACGATGGAAGCGACGTACATGTGGAACTAAAT
                                                                                                                                                                                                                                                                                                                                                      AAGTTGTATCATGATGACCCCTGTTTTTAATCCTCTGACTCCTTGGGAGAGACCACCTATA
                                                     GTTGATCATGAGCATGGGTCAGACATCATAGCTAACATGACAAAAGCACCAAGGGTTAAG
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2277 GAAATATTGCTCATCATCACCACCACCACCACCACACCA		349 uSerPheThrAlaArgGluLeuAlaAspGlyThrLeuPheLysAlaIleGluAspTyrAs 	2038 AACAAAAGTTTCACCCAAGAATGTTCACTCTCATATTTCGTTCCTTTGATGTGTATCCATC 2097 330 -ValThrGluThrAlaLeuValAssnMetThrSerMetGluCysGlyLeuProThrLeuLe 349	320 eIleAsnIleGluIleProSerThrSer	300 gValTyrHisCysAspGluGluGluTyrGlnSerLysTyrSerGlyTrpProThrAsnII 320 	1799 TCGGTTGTTGTCCAATTCTTTTGCGTCGTCATTGTGGCTATGCCALITICAAAGAATAG 1898 280 SLYSG1YASPASDThrSerTrpThrHisPheSerG1YG1YAlaAlaLySLYSASPLYSAr 300	CATGTGACATATTGACATGCGCTTCTCATGTTTTTTGTTGGCAAGGCTTCAGGGAACTGC 179 aArgLeuLeuSerAsnSerPheAlaSerSerLeuTrpLeuMetProPheSerLysAsnCy 280	1679 GAGAAGAAACTTTGACTGAAATCTTTTATTTAATAGGCTATGATTTGTTTATTGAAAT 1738 258GlyThral 260	257 257 1619 TACAACCACATGTACACTGATTTAGTTTTCAGATTATTATGGTAGACTTTAAGTT 1678 257	99 TITIGARAGIATTACITTITGITARITIGAACIIGCIGIACGCGGAIAIGGIAICIGIAGAICIIG	9 CTTCTCTTTAGTTTTAAGTAGTTGATATCAACCAGGTCTTATAACTCACTGGATTTTCCT 14 7 25	41 alleLysSerThrLeuSerGlyValThrPheGlyLeuProValSerGlu	232
Qy 464V 464 Db 3417 GTACACTGCAATATTGACTCTCCGCTACTTTTATTGATTATGAAATTGATCTCTTATAGG 3476 Qy 464 alprotyrHisSerLeuSerTrpCysLysAsnTrpLeuGlyProLysValAsnIleThrM 484	Db 3297 TĞGACCTATAACTGGGGATGAGACGGTAAGCTCAGAAGTTGGTTTTGAAATTATCTTCTT 3356 Qy 463 463 Db 3357 GCAAACTACTGAAGACTAAGATAATTACTTGCTTCTGGAACACTGCTTGCT	446	445	3057 TTT 445	Db 2997 TCTAGTGGCATGTTATCTCAGTTGCATAAGCAAATTATTAAACAACTAAAATTTAAGTAC 3056 Oy 445	444 lse 2937 GTC	424 2877	Qy 415	2697 414	Qy 396 uArgProProIleLysAsnValPheCysIleTyrGlyAlaHisLeuLysThrGlu 414	Db 2517 TGACTAATAGCGTCAATFTFGTFTFTCTAGCAAATCTTTGTGAATTATATATATATATCT 2570 Qy 383TyrhisAspAspProValPheAsnProLeuThrProTrpGl 396	382 2457 AGTTA 382	Qy 382 382 Db 2397 GAAACCTTATTATTGATTATCAGTTCTCTCCTTATATTATGGAATGTCTTTTTCGTTTAC 2456

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                                   Banas, A., Stahl, U., Stymne, S., Lenman, M., Ronne, H. and Dahlqvist, A. A new class of enzymes in the biosynthetic pathway for the production of triacylglycerol and recombinant dna molecules encoding these enzymes encoding these enzymes Patent: WO 0060095-A 11 12-OCT-2000; BASF PLANT SCIENCE GMBH (DE); BANAS ANTONI (PL); STAHL ULF (SE); STYMNE STEN (SE); LENMAN MARIT (SE); RONNE HANS (SE); DAHLQVIST ANDERS (SE)
                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Banas, A., Stahl, U., Stymne, S., Lenman, M., Ronne, H. and Dahlqvist, A. A new class of enzymes in the biosynthetic pathway for the production of triacylglycerol and recombinant dna molecules encoding these enzymes
Patent: WO 0060095-A 30 12-OCT-2000;
                                                    Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e-mail for correspondence: arab@sequence.stanford.edu
Genes with similarity to proteins in the databases are described as
'putative', '-lke' or 'similar to'. Genes that have EST
similarity but no significant protein similarity are described as
'unknown proteins'. Genes that are annotated based only on gene
prediction software are described as 'hypothetical proteins'.
The software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
http://compbio.ornl.gov/section/index.html), GENSCAN (Chris Burge,
http://gnomic.stanford.edu/~chris/GENSCANW.html), Fexa (V.Solovyev
& A.Salamov, Sanger Centre, http://genomic.stanford.edu/~chris/GENSCANW.html),
Bender (S.M. Hebsgaard, et al., CBS, Technical University of
Denmark, http://www.cbs.dtu.dk/NetPlantGene.html).
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Submitted (30-DEC.1998) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                On Dec 30, 1998 this sequence version replaced gi:2734094.
Bases 1-9262 of clone F21M11 overlap with bases 68998-78259
'TAMU' BAC clone F20D22 (AC002411) and bases 119525-119914 c
F21M11 overlap with bases 1-389 of 'TAMU' BAC clone F21B7
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Pederapiel, N.A., Palm, C.J., Conway, A.B., Kurtz, D.B., Conway, A.R., Au, M., Araujo, R., Buehler, B., Dewar, K., Feng, J., Kim, C., Li, Y., Oji, O., Osborne, B.I., Shinn, P., Sun, H., Toriumi, M., Vyotskaia, V., Yu, G., Ecker, J., Theologis, A. and Davis, R.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AC002560)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 119914)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 119914)
                                                                                                                           1. .7000
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entry, AC002411."
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                                                                                                                                                                                                                    /note="overlap with F21M11."
                                                                                                                                                                                                                                                                                                              ecotype="Columbia"
                                                                                                                                                                                                                                                                                                                                             'clone="F21M11"
                                                                                                                                                                                                                                                                                                                                                                           'chromosome="I"
                                                                                                                                                                                                                                                                                                                                                                                                       mol_type="genomic DN/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Arabidopsis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ocation/Qualifiers
                                                                                                           .1091
                                                                                                                                                             in
                                                                                                                                                                                                                                                         bases
                                                                                                                                                             region
                                                                                                                                                                                                                                                         68998-78259
                                                                                                                                                                   are
                                                                                                                                                                   annotated
                                                                                                                                                                                                                                                         of 'IGF'
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                                                                                                                                                                                                                                                            BAC clone
                                                                                                                                                                   the F21M11
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clone

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13033. .14514
/gene="F21M11.2"
join(13033. .1348
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apykuldaifdeadagsteknkkeeekkkerskasravatergerkafeelyddee

ddydedeffylkriksgrassssssssynnedlktofeeeddddystelfelkry

vrngerglekolamyynnaspssssssssssynnedlktofeeeddddystelfelkry

vrngerglekolamytynnaspssssrlknepeevppmyllpahymetkydsasalvilnd

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rkqvlrfceecflerakkveilepckghlkrgaikecmfkcggtrggrvudgrmhu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MDRTMFLSLTIASLLVGVVSAGDWNILNQLRGLGSSSSQNGIVS KGIKTDLKGYCESWRINVEVHNIRKFDVVPQECVSHIKDYMTSGQYKDDVARTVDEVI LHFGSMCCSKSKCDGMDANIFD1DDTTLJSTIFYHKKNGFFGGBKLNSTKFEDMTQKKK AFAVPHNKKLTYIDIREBGIKIFLISSRKEYLRSATVDNLIQAGYYGWSNLMLRGLEDQ QKEVKQYKSEKRKMLMSLGYRWGVWGDQWSSFAGCPLPRRTFKLPNSIYYVA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="F21M11.2"
join(13061. .13480 ...
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FESEYDAANHTPESYTEQAAKNVRDITASEQPSNAARKRICGDSFIQESSPNPKTQDP
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                                                                                                                                                                                                                                                                                                                   complement (16835. .20238)
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complement ()oin (16835. .17185,17274. .17392,17491. .1765
17795. .17885,17982. .18079,18175. .18361,18504. .18604,
18705. .19049,19134. .19349,19439. .19791,19862. .19967,
20188. .20238))
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WGSEERLEGDKALCLDGMFYGNISRFLNHRCLDANLIEIPVQVETPDQHYYHLAFFTT
RDIEAMEELAWDYGIDFNDNDSLMKPFDCLCGSRFCRNKKRSTKTWQILNKA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAVDASLSTWLSTSESGSECNSASMYTLTPEKLKSTSCYSKPLRINHDDRPVLCALTLEDIKQFSATSTPRKSPSKSPDETPIIGTVGGYWGNRSKAIDCGSASSFKGIPNTSSKYREDKSVNWHSTPPEARLEKALNNIDK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /proteIn_id="AAD10667.1"
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DSLHNPTKEVYTQDIGDKTEEIDSKLRRSNETVRDGNHYDGQGYLNPVENLTQWKSAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Unknown protein; Location of ESTs 40C3TT.gb|AA728590 and40C3T7, gb|T04573"
/codon_start=1
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16327. .16362))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15906. .16006,16327. .16362))
/gene="F21M11.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (14004. .16362)
/gene="F21M11.3"
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/note="Similar to acid phosphatase; Location of ESTs
,110C2T7 , gb|T42036, and 110C2XP, gb|AI100245"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="AAD10665.1"
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/gene="F21M11.1"
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SHTEQDSKRKRDITASDAMENHLKVPKRENNLMQKSADIDCNGKCSANSDDQLSEKIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SKGRTKQKQSQKENSNFIADQEEKRDSSSFGTDPQIDDITLSVKPKCRIEPKKLRNQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16327. .16362))
/gene="F21M11.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (join (14004. .14312,14565. .14641,14787.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="AAD10666.1"
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                                                                                                                                                                                                                                                              /gene="F21M11.4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      codon_start=1
                                                                                                                                                                                                                                      codon_start=1
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DB:
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Best Local Similarity:
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gene

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US-09-651-651-5 (1-546) x AC003027 (1-119914)
                                                                                                                                                                                                                                                                                                                                                    LeuserGlyIleIleProGlyPheAlaSerThrGlnLeuArgAlaTrpSerIleLeu
                                                                                                                                                                                                                                                  ATTTGCGGTGGCCGAACTGCGGTGGAGGATGAGACCGAGTTTCACGGCGACTACTCGAAG
                                                                                                                                                                                                                                                                                     IleCysGlyGlyArgThrAlaValGluAspGluThrGluPheHisGlyAspTyrSerLys
                                                                                                                                                                                                                                                                                                                                                                                  MetGlyAlaAsnSerLysSerValThrAlaSerPheThrVallleAlaValPhePheLeu
                                        GACTGTCCATACACTCCGTTGGACTTCAATCCGCTCGACCTCGTATGGCTAGACACCACT
                                                                                         AspCysProTyrThrProLeuAspPheAsnProLeuAspLeuValTrpLeuAspThrThr
                                                                                                                                                CTATCGGGTATAATCATTCCGGGATTTGCGTCGACGCAGCTACGAGCGTGGTCGATCCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MNTKIMRLPPRRVLTADKRKERDAFISSVTDNPPEIAKFPSPPP
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KIKPSHTVEPAEECEPKRKRYEEVANLLRSDGAQLPGIVNPAQLARFLKL"
complement (29264..32033)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="mgansksytasftylayffllcggrtayedetefhgdysklsgl
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ptklebrdlyfhklkiffetalklrggbslykabenkwebfgleanatyakpkhyl
kwldohihayfaygapllgsyeaikstlsgytfglpysegtaallsnsfasslwimpf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               join(20752. .20994,21362. .21497,21596. .21740,21825. .21994,
22102. .22178.22542. .22758,22920. .23064,23343. .23442,
23599. .23693,24021. .24072,24227. .24298,24441. .24647)
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/note="Hypothetical protein"
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27777. .28734
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HEHGSDIIANWTKAPRVKYITFYEDSESIPGKRTAVWELDKSGV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SKNCKGDNTFWTHFSGGAAKKDKRVYHCDEEEYQSKYSGWPTNIINIEIPSTSARELA
DGTLFKAIEDYDPDSKRMLHQLKKYVPFFVIRNIAHRSSLAGFLLYHDDPVFNPLTPW
ERPPIKNVFCIYGAHLKTEVGYYFAPSGKPYPDNWIITDIIYETEGSLVSRSGTVVDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (join (29264. .31015,31312.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="AAD10668.1"
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41.58%
41.58%
78.65%
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Matches:
Conservative:
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Indels:
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217 rLeuLysTrpLeuAspGlnHisIleHisAlaTyrPheAlaVal	21771 CTTCTCTTTTATGTAAGATAAGCTAAGAGCTCTGGTCGTCTTCCTTTTTGCAGGTTGAC 21830 177 rPheGluThrAlaLeuLysLeuArgGlyGlyProSerIleValPheAlaHisSerMetGl 197	eGlualaaanalaIleValAlaValProTyrAspTrpArgLeuSerProThrLysLeuGl 	TTCAATTTGATATCATCTTGTTGTGATATATATGGCTAAGTTCATTAATTTGGTCAATTGlyproleuserThrValTrpLysGluTrpLeuLysTrpCysValGluPheGlyIl	98 rAsnGlnThrAspHisProGluCysLysSerArgProAspSerGlyLeuSerAlaIleTh 118	21292 GGTCATTITACTTGTGCATTGTGATTCTTTTGGTTGTTGCTTACTGATCGACGTGATGGA 21351 82LeuleuSerÄläVäläsnCysTrpPheLysCysMetVälLeuäspProTy 98	81 81 21232 TTTTTATTCAACTAGATCTGCAAGTTTTTCAGAGTGCTCAATAGTAGTTAGAAAATGTTA 21291 81 81	GTCAACAGTGACGCTTCTGAATCTGAGTTTAGAGTCATATAAAACAGCTGACTCGGCGAG	81
23028 GAAATATTGCTCATCGATCATCACTTGCTGGCTTCTTGTACGTCAAATTGTTTGT	Db 22849 aGTTACAGAAACAGCTCTTAGTCAACATGACCAGCATGGAATGTGGCCTTTCCCACCCTTTT 22908 Qy 349 uSerPheThrAlaArgGluLeuAlaAspGlyThrLeuPheLysAlaIleGluAspTyrAs 369	QY 320 6116A8B1116G1U1LEFTOSETITESET 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	280 slysolyaspasninsertrythhispheserdlyGlyalaAlaLyslysasplysar	22490 CATGTGACATATTGACATGCGCTTCTCATGTTTTTTTTTT	257	22310 257	Db 22190 CTTCTCTTTAGTTTAAGTAGTAGTAGTCAACCAGGTCTTATAACTCACTGGATTTTCCT 22249 Qy 257 257 Db 22250 TTTGAAAGTATTACTTTTGTTAATTGAACTGCTGTACGCGATATGGTATCTGTAGATCTT 22309 OV 257 257	241 alleLysSerThrLeuSerGlyValThrPheGlyLeuProValSerGlu

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/8787	ACCCTATCATTCACTCTCTTG3TGCAAGAATTG3CTCG3ACCTAAAGTTAACATAACA	ď
4 6	464 alProTyrHisSerLeuSerTrpCysLysAsnTrpLeuGlyProLysValAsnLleInrw	. 8
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24227	24168 GTACACTGCAATATTGACTCTCCGCTACTTTTATTGATTATGAAATTGATCTCTTATAGG	문
464	464	ş
24167	24108 GCAAACTACTGAAGACTAAGATAATACTTGCTTCTGGAACACTGCTTGCT	90
463	463	Ş
24107	TATAACTGGGGATGAGACGGTAAGCTCAGAAGTTGGTTTTGAAATTATCTTCTT	Ф
463	455 aGlyProIleThrGlyAspGluThr	8
24047	ი-	뫄
455	446ArgSerGlyThrValValAspGlyAsnAl	γQ
23987	23928 AATTTCATATTATTAGGAGTAGTCGTGCTTTTAAAAAATTTTGTTTTAAGAAACCGAAAAA :	DЪ
445	445	ş
23927	23868 TGCATGAAACATGACACTTGTATCAAAGATAACTAGCAAAACAAAC	망
445	445	Ş
23867	23808 TTTTTTATCATTCCTTTTGAGCTTAGTGGATGATCAGTGGCTTAAAGTGGGAAGAGGTGT :	ф
445	445	ş
23807	23748 TCTAGTGGCATGTTATCTCAGTTGCATAAGCAAATTATTAAACAACTAAAATTTAAGTAC	Db
445	445	Ş
23747	 CAAGGTAATTTTCCGCAATGGCAGAAGTAAAACAGGAAGGCAAAGTCTTCTGTATCAG	, pp
445	444 Ser	Ş
23687	23628 ACCTTATCCTGATAATTGGATCATCACGGATATCATTTATGAAACTGAAGGTTCCCTCGT	ф
444	rProAspAsnTrpIleIleThrAspIleIleTyrGluThrGluGlySerLeuVa	Ş
23627	23568 GGTACTAAATGTATGAAGCTGTCTGTCATAGGTTGGTTATTACTTTGCCCCAAGTGGCAA	Db
424	Y-Ly	Ş
23567	23508 AATATCTTTTTGAATTATGATTTATCTTCTCCCTTGCATCTTATGCTATTAAGCGTTAAA 2	Db
414	414	δ
23507	23448 ATGCATTCTCAATATCACATTATGCGTTGACTTTGTTATTATATTCCCCCATTTGGTTTGC 2	망
414	414	Ş
23447	CACCTATAAAAAATGTATTTTGCATATATGGTGCTCATCTAAAGACAGAGGTATG	В
414	396 uArgProProIleLysAsnValPheCysIleTyrGlyAlaHisLeuLysThrGlu 4	Ş
23387	23328 AACTATACTTTTCAGGTTGTATCATGATGACCCTGTTTTTAATCCTCTGACTCCTTGGGA 2	망
396		છ
23327	23268 TGACTAATAGCGTCAATTTTGTTTTTCTAGCAAATCTTTGTGAATTATATATA	망
382	382 3	Ş
23267	23208 AGTTATGAATGCAAAAGGGGGTATTTTAGTTGATTGATTCTCTCATTCTCTAGTTTGTTT	망
382	382 3	ş

CDS	RESULT 8 AP493159 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL PUBMED REFERENCE AUTHORS TITLE JOURNAL FEATURES FEATURES FEATURES SOURCE	2
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GluAlaAsnAlaIleValAlaValProTyrAspTrpArgLeuSerProThrLysLeuGlu
                                                                                                                                              ProLeuAspPheAsnProLeuAspLeuValTrpLeuAspThrThrLysLeuLeuSerAla 85
                                                                                                                                                                                                                                                                                                            GAAGCCTCCGCGAAAGGCGGCGAGTTCACCGGGGACTACCCCAAGTTGTCCGGAATCATA
                                                                                                                                                                                                                                                                                                                            ThrAlaValGluAspGluThrGluPheHisGlyAspTyrSerLysLeuSerGlyIleIle
                                                                                                           CysLysSerArgProAspSerGlyLeuSerAlaIleThrGluLeuAspProGlyTyrIle
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                                           ACAGGTCCTCTGTCCTCAGTGTGGAAAGAATGGGTTAAGTGGTGCGTTGAGTTTGGTATA
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                                                                                             TGCAAGTCTCGACCTGATAGTGGTCTTTCCGCAATTACAGAACTTGATCCAGGTTATATA
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SPSKLEERDLYFHKLKLTFETALKLRGGPSLVLAHSLGNNVFRYFLEWIKLEIPFKQY
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WLQWWHDTRPDATSKFVYKAKRGPLRDEDCYWDYGKARCAWPEYCEYRYNFGDVHLGQ
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    CTGAATGTAGAACATCAAGAAGAAGCAGACATTGTTCCCAACATGACAAGGTCACCAAGG
                                                                        LysValAsnIleThrMetAlaProGlnProGluHisAspGlySerAspValHisValGlu
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1000001 1000001 2000001 2000001 6000001 6000001 9000001 10000001 1100000001 1100000001 1100000000	TyrlleThrPheTyrGlu ::: TACATAACCTATTATGAA LeuAspLysSerGlyTyr ::: CTTGATAAAGCAAATCAC
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1.0	17   07	Indels: Gaps:	15	Query Match: DB:
		Mismatches:		Best Local Similarity:
105922 ATGCTGCACGATTCATCAGCAATGTGATAGATTGTGA		Matches:	1483.50	'n
126	110000 Qy		7.3e-116	Alignment Scores: Pred. No.:
105982 TTATATGCCTCGCTTAATTCTCCTTGGTATTGATTGC	Db	971000		AP008208_196
126	Q	99	950000	AP008208_194 AP008208_195
106042 AGGCCTGACAGTGGTCTTTCTGCAATTACAGAGTTAA	Db	1000	19200001	AP008208 192 AP008208 193
		911000	19000001	AP008208_190
106102 TgCTCAAATGCATCGCTCAACCAG2	Qy	881000 891000		AP008208_187 AP008208_188 AP008208_189
106162 CATTTTCATACTTGCGACTTAATCGGGTTCATGGTGC	מס	861000 871000	18500001	AP008208_185 AP008208_186
82	γ0	18410000	18300001	AP008208_183 AP008208_184
106222 GAACAGGCTGTAACGATTATATTTGTTACATGTAGGC	Db	18210000	18100001	AP008208_181 AP008208_181
81	QY	18010000	17900001	AP008208_179
106282 GTAAGGCGTCATACGGCTTAATTGGGTGAGGTTGTTA	Db	17810000	17700001	AP008208 177
81	QY	17610000	17500001	AP008208_175
106342 GTCATTACTTCACTGGAAAAGGGATATTTGTTAATTG	Db	17410000	17300001	AP008208 173
81	Qy	17210000	17100001	AP008208 171
106402 CGGTTGTGTGTACTACGTAACCATGCTAAAACTAGTG	Db	17010000	16900001	AP008208_169 AP008208_170
81	Qy	16810000	16700001	AP008208_167
106462 ATCTGCTTGATTTGAGTGACCATCTAGTTATAGGTTT	Db	16610000	16500001	AP008208_166
81	γ	16410000	16300001	AP008208_163 AP008208_164
106522 TTGATGGATTAAAGTAATTTTGCAATGGCCCATCAGG	Db	16210000	16100001	AP008208_161 AP008208_162
81	VQ	16010000	15900001	AP008208_159
106582 TGGATAATATATGTGCTTTTGTTCTTTTATTAGGATT	Db	15810000	15700001	AP008208_157 AP008208_158
81	γ	15610000	15500001	AP008208_155 AP008208_156
106642 CGTTCCGTACTGTCCTCCTGATATTCAGAAAGCTACT	D. D.	15410000	15300001	AP008208 153
81	γ	15210000	15100001	AP008208 151
106702 TTCGACTTCAACCCCCTCGACTCCGTCTGGCTCGACA	Db	15010000	14900001	AP008208_149 AP008208_150
67 LeuAspPheAsnProLeuAspLeuValTrpLeuAspT	Qy	14810000	14700001	AP008208 147
106762 CCCGGGTTCGCGTCGACGCAGCTGCGCGCGTGGTCTG	Db	14610000	14500001	AP008208_145
47 ProGlyPheAlaSerThrGlnLeuArgAlaTrpSerI	δλ	14410000	14300001	AP008208_143 AP008208_144
106816 GGAGGCGATGGCGGCGGGATTTCĠACTACC	מס	14210000	14100001	AP008208_141
27 AlaValGluAspGluThrGluPheHisGlyAspTyrS	Qy	14010000	13900001	AF008208_139 AF008208_140
106876 TCGGTGGCGGTGGCGGTGGCGGTGGCGGTGGCGG	Db	13710000 13810000	13600001	AP008208_136 AP008208_137
7 SerValThrAlaSerPheThrValIleAlaValPheP	Qy	13510000	13400001	AP008208_135 AP008208_135
9-651-651-5 (1-546) x AP008208_348 (1-110000)	us-09-	13310000	13200001	AP008208_132 AP008208_133

126	5	Qy 126	_
105863	ATGCTGCACGATTCATCAGCAATGTGATAGATTGTGATTTATGCTTCAACTCCCATGCAA	Db 105922	_
126		Оу 126	_
105923	TTATATGCCTCGCTTAATTCTCCTTGGTATTGATTGGATTATTGAATTTTGAGTACAAAT	Db 105982	_
126		Оу 126	
126 105983	ArgProAspSerGlyLeuSerAlaIleThrGluLeuAspProGlyTyrIleThr	Qy 109 Db 106042	
106043	TrpPheLysCysMetValLeuAspProTyrAsnGlnThrAspHisProGluCysLysSer	Qy 89 Db 106102	
88 106103		Qy 82 Db 106162	п о
106163	GAACAGGCTGTAACGATTATATTTGTTACATGTAGGGGGTCATATTTAAGTATTATCTTT	1062	
81			^
106223	GTAAGGCGTCATACGGCTTAATTGGGTGAGGTTGTTACAGAAGCATTCAATCTGTGCAAT	ДУ 81 Db 106282	
106283	GTCATTACTTCACTGGAAAAGGGATATTTGTTAATTGTGATGGTTGGGACTGTTTTCCT	1063	
81		Qy 81	_
106343	CGGTTGTGTGTACTACGTAACCATGCTAAAACTAGTGACACGTTCAGTTAGAAGAGGTTT	Db 106402	н
81		Оу 81	_
106403	ATCTGCTTGATTTGAGTGACCATCTAGTTATAGGTTTTTGGAAGTGTTTTTAGGACTAAAT	Db 106462	-
81		Qy 81	^
106463	TTGATGGATTAAAGTAATTTTGCAATGGCCCATCAGGCAGATGCGTGTGTGCGACTGCAC	Db 106522	
81		Qy 81	
106523	${\tt TGGATAATATATGTGCTTTTGTTCTTTATTAGGATTCGTTGGTCTGTTCTTGTGAGGCA}$	Db 106582	н
81		Qy 81	0
106583	CGTTCCGTACTGTCCTCGATATTCAGAAAGCTACTTTTGCTAGTAACTGTTGTTC	Db 106642	н
81		Qy 81	0
106643	TICGACTTCAACCCCCTCGACTCCGTCTGGCTCGACACCGCCAAGGTCAGAACCACCCCT	1067	
81	LeuAspPheAsnProLeuAspLeuValTrpLeuAspThrThrLys	Qу 67	0
66 106703	ProGlyPheAlaSerThrGlnLeuArgAlaTrpSerIleLeuAspCysProTyrThrPro	Qy 47 Db 106762	п О
46 106763	AlavalGluAspGluThrGluPheHisGlyAspTyrSerLysLeuSerGlyIleIleIle ::: :::	Qy 27 Db 106816	ם מ
106817	TCGGTGGCGGTGGCGGTGGCGGTGGCGGTGGCGGCCGTGGGCGGTGGGC	Db 106876	ы
26	erValThrAla		Ω
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378 GlnLeuLyslysLeu	Q	239 alGluAlaIleLy8SerThrLeuSerGlyValThrPheGlyLeuProValSerGlu 257        :::   :::
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	B 5	224 iBileHiBAlaTyrPheAlaVal
7 7	) b	204 heLeuGluTrpLeuArgLeuGluIleAlaProLysHisTyrLeuLysTrpLeuAspGlnH 224              :::
	o a	184 euArgGlyGlyProSerIleValPheAlaHi8SerMetGlyAsnAsnValPheArgTyrP 204                105022 TTCGAGGAGGGCCTTCTTTAGTGTTTGCTCATTCCATGGGTAATAATGTGTTTTCGCTACT 104963
320 LelleAenlleGluileFroserinr-Serval	Q & Q	
STyrSerGlyTrpProThrAsnI                       ATACTCAGGATGGCCCACAAACC	dg Qy	175 05142
283 gpAsnThrSerTrpThrHisPheSerGlyGlyAlaAlaLysLysAspLysA 300	B Q	175
	Qy Oy	CATGCAAGCTGAAATTGATAATTTTTTTTGCGGGGGAAATTGATAAGCTTTTACTTGCTT
258	B 8	175
GTTGAATCTGTACTTAGCTATATATTGCCAAAATTGTTACATTA	Db	175
104362 CAGTTAGGGAAGGTTGTTTTGGTGGATGTATAAATTCTCTACCTTCGAGTGATACACATGT 194303	Q B	TCACTGCCCATTGGCTTTCGATAGTATTTGATGTTATTACTAATAATTGGTGTAAAAACA
257	. 8	105502 GTACTTCCATAAATTAAAGTTTGTAACACTTCACTTCATATCACATAGCAATCAAT
ACTTCTCATAGCCGATTCGCACGGCCAGGTTGTGTGCCACAACCATGCTAGTTTTAGAGT	Db .	uTyrPheHisLysLeuLys175
104482 CTTCTACACGTGCAAGGGAACCTTTTAGTACTGTTGGAGTCTTGGAGACAACAATGCCTT 104423	OV D	149 #11evalAtavalrIO1yrAspitpAtyleGeterio11111ysusgustustustustustysusgustustustysusgustustysusgustustysusgustustysusgustustysusgustustysusgustustysusgustustustysusgustustustysusgustustustysusgustustustysusgustustustysusgustustustysusgustustustysusgustustustustysusgustustustysusgustustustysusgustustustysusgustustustysusgustustysusgustustysusgustustysusgustustysusgustustysusgustustustysusgustustysusgustustysusgustustysusgustustysusgustustysusgustustysusgustustysusgustustysusgustustysusgustustysusgustustysusgustustysusgustustysusgustustysusgustustysusgustustysusgustustysusgustustysusgustustysusgustustysusgustustysusgustustavaltavaltavaltavaltavaltavaltavaltava
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TTGCCCCTTGTTCTTTGTCCCTGCCCTTTCTGAGAGTACTGTTCTGGTAACCTCTCAGCC	D 4	USerThrValTrpLysGluTrpLeuLysTrpCysValGluPheGlyIleGluAlaAsnAl 149
104602 GTCCAATACTGAATAGTTTTTATTTCCTTTTTGGATTCACTAGGTTTTTGTGGTGATTCTT 104543	<u> </u>	AGCCATAAAAAAATCTTTCTTACTAATTTGGTTTTATTGGCCAAGTTTTCAGGTCCTCT
257 257	Q	GITCATCGGIAAGCTGIAGAAITCCCCAICI
104662 TGATATTTATACATTTTTCCTCCAACATTGTTAGTGTTGAATTTAAGTATGTTGTTTGGTT 104603	Db	126
	δ 8	105802 GAGTTAATAATGGATATTGCCATGAGAATAATAGCATTAGCTAGGTTACATTGCAAATTC 105743
257 257 104722 GOCUMUTATIGAR TURTESTETTUTCARTRATICTOCTTTTCCTCTCACGACGCTATATTTC 104663	β δ	105862 TGGAAAAAAAAACCATCGATGGCAAGTGAGAGTGATAAAATTTGACATCAAGCTTTTGT 105803
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Db 4962 TTCTGGAATGGTTGAAACTAGAA Qy 224 isIleHisAlaTyrPheAlaVal	204	Db 5022 TTCGAGGAGGGCCTTC	Qy 184 euArgGlyGlyProSe	5082	176	5142	175		175	5262	175	5322	175	5382	175	5442	Qy 175	5502	169	5562	149	Cy	1 0		127	126	5086		156	5862	126	5922	126	5982	Оу 126
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3894 TGTTTTCCTCTGGCAGATACGGAAGCATACCCATCCATTATGGATACAACTGAGAACATA 3835 339 ThrSerMetGluCysGlyLeuProThrLeuLeuSerPheThrAlaArgGluLeuAla 357	337AsnMet	331 336	320 leIleAsnIleGluIleProSerThr-SerVal	300 rgValTyrHisCysAspGluGluGluTyrGlnSerLysTyrSerGlyTrpProThrAsnI 320	283 spasnThrSerTrpThrHisPheSerGlyGlyAlaAlaLysAspLysA 300	263 euSerAenSerPheAlaSerSerLeuTrpLeuMetProPheSerLysAsnCysLysGlyA 283 ::     :::	258	257 257 4302 GTTGAATCTGTACCTTAGCTATATATTGCCAAAATTGTTACATTATATGCCATCTTATAAT 4243	257 257 4362 CAGTTAGGGAGGTTGTTTTGGTGCATGTATAAATTCTCTACCTTCGAGTGATACACATGT 4303	257 257 4422 ACTTCTCATAGCCGATTCGCACGGCCAGGTTGTGTGCCACAACCATGCTAGTTTTAGAGT 4363	257 257 4482 CTTCTACACGTGCAAGGGAACCTTTTAGTACTGTTGGAGTCTTTGGAGACAACAATGCCTT 4423	257 257 4542 TIGCCCCTIGITCTIGITCCCTGCCCTTTCTGAGAGTACTGTTCTGGTAACCTCTCAGCC 4483	4602 GTCCAATACTGAATAGTTTTTATTTCCTTTTTGGATTCACTAGGTTTTTGTGGTGATTCTT 4543	TGATATTTATACATTTTTCCTCCAACATTGTTAGTGTTGAATTTAAGTATGTTGGTT	GCCTTTATGAATTATATATTTTTCAATAATGTGTCCTCTGCCCTCAGGAGGCTATATTTC	alGluAlaIleLysSerThrLeuSerGlyValThrPheGlyLeuProValSerGlu       :::   :::	
Qy 463ThrValProTyrHisSerLeuSe 470	Db 2816 AGCCCAACAATTCCAGCGGAAGACGGTATGTTCTACTGTAGTATCTTTATAGGTCA 2757	2876 TTTAGAATAAAATAGTAACACAATTTATTCTTTCCAGATCAGGTAATTCTGTTACTGGAA	CY 460 YABOULD 102  [	455AIRGLYPROLITINGL 2996 ATAATAGCTTTTCGTGCATTTGTTTTCTCGAAAAATACTGACCTTTGAACCTTTGGCTTT	447	3116 TATTTTTTTGCTTTAATATGAAAAGATATTTGTAGTTCGCAGACTCATTTTTCATGGC	3176 TCAAATTATCCATTATCTGTCTTATGTATGTCTGCTTCTAGTGTAGTTTCCTGGAACAG	w		3356 ATTACCATTCACCGATTTATGGCCTTTTTGTTAAGCAGGTAGGCTATTATTTTGCACCG	3415 GT-ATGATTGGGATTTTTCTTTGATTGTTAAAGTTTCTACTTTAGCCTGCTTTGAACCAC	W	3535 395	Db 3595 TATGCTTATGGAAGTAAATATGTGTGATTTTGATTAAATTGTATCTAATACCCCCACACTT 3536  Qy 383TYrHisAspAspProValPheAsnProLeuThrPro 394	Db 3655 AATTCTCAGTTTCACATACATATTTATCTTCAAAGTAAACCACCAACTTACATGTTTTTA 3596 Qy 382 382	OY 3.6 STITLED LYBER 1902	3834 ACATCCAGCATGGAGTGTGGAAAGCCAACTCTTTTGTCATTTTCTGCTAGGGAGGTTTCA 358 AspGlyThrLeuPheLysAlaIleGluAspTyrAspProAspSerLysArgMetLeuHis

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KEYWORDS
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
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Direct Submission

AL Submitted (29-AUG-2001) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan [2-1-2, Tsukuba, Ibaraki 305-8602, JuRichttp://rgp.dna.affrc.90-1, Ibaraki 305-8602, Japan [2-1-2, Tsukuba, Ibaraki 305-8602, Julian [2-1-2, Tsukuba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa (japonica cultivar-group)
BAC clone:OJ1293_E04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sasaki, T., Matsumoto, T. and Yamamoto, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Publ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sasaki, T., Matsumoto, T. and Yamamoto, K. Oryza sativa nipponbare (GA3) genomic DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone:0J1293_E04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AP004120.3 GI:47847857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aProArgValLysTyrIleThrPheTyrGluAspSerGluSerIleProGlyLysArgTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AACAAAGATGAATGTCGACCACCATGTAGGCCAGGGCATACTCCCAAACATGACGAGGAC 2397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sValGluLeuAsnValAspHisGluHisGlySerAspIleIleAlaAsnMetThrLysAl 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTTTCCTGCTTTGTACATCCTACTGTTTTTGCAGGCAGAACATGATGGATCTGATTTACA 2457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTGTTGTGGCTAATAGAATTATTGACTGTTTCCTTGTAGCATATCACAATGTTAATGTGC 2517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCATGTGCCTAGTGATATGATCCTCAGCAGAGGAGTTTGAGGCCCTGTTTATTAATTTGTT 2577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGGTGCAAGAACTGGCTTGGGCCAAAAGTGAACATAACTAGGGCTCCGCAGGTATTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rTrpCysLysAsnTrpLeuGlyProLysValAsnIleThrMetAlaPro-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGCCGTCTGGGAGCTTGATAAAGGTGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      545
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genomic DNA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . 536
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FEATURES
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The orientation of the sequence is from -2NM13 to M13rev of the BAC clone. This sequence of OJ1293_EO4 clone has an overlap with OSAUBBAOS3LI1 (DDBB: AP005691) clone at 5' end and with P0643F09 (DDBJ: AP005111) at 3' end. The sequence was generated by combining Monsanto and RGP-dapan sequencing data. Detailed information on or tring entry maility troopther with annotarion of this entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://rgp.dna.affrc.go.jp/GenomeSeq.html.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       overlap and assembly quality together with annotation of this is available at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   join(6482. .6988,7071. .70

8501. .8573,8672. .9312)

/gene="0J1293_E04.2"

join(6482. .6988,7071. .70

8501. .8573,8672. .9312)

/gene="0J1293_E04.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="melroncvokigdskvpwkfvpdfpfsevvefikgyrvevcgki
pckmlsgnsnyaayivfvvaedscglasvwvatvgvggrostrovcldssnrndyyye
geievpodgsvilpoeradgmmelelgefynoegnnogevcfslvkpkagrmlsnggl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="O11293_E04.1"
join(<1863. .T936,2024. .>2468)
jene="OJ1293_E04.1"
/note="start and end point are not identified"
join(1863. .1936,2024. .2468)
/gene="OJ1293_E04.1"
                         /translation="meeegeglceiarlpeellsaaisrasprdachaaavspapraa
Adsdawasflprilfedladgelspapaskeelflresggpylledraksmwldrest
Akcymlsarslviingotphywrwipltdsraseagaelldvcwleirgrikskwlspu
Styaaymvfkiadefygldapfqeasvslggrgstkivcvqsydsedeevpenywpms
                                                                                                                                                                                                                                                                      contains full-length cDNA(s):
phloem-specific lectin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="supported by full-length cDNA(s):
join(11953..12242,12368..12486,13292..
/gene="OJ1293_E04.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="hypothetical protein"
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/db_xref="GI:47847858"
                                                                                                                                                                                                                                                                                                                                                             /note="supported by full-length cDNA(s):
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/gene="OJ1293_E04.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="0J1293_E04.3"
join(11875. .12242,12368. .12486,13292. .13972)
/gene="0J1293_E04.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="transposase-like"
11875. .13972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VIQGIEIRPKIS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="predicted by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol type="genomic DNA"
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/db_xref="taxon:3947"
/chromosome="2"
                                                                                                                                                /protein_id="BAD21652.
/db_xref="GI:47847859"
                                                                                                                                                                                   /product="F-box family protein-like"
/protein_id="BAD21652.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Oryza sativa
|GPLLRRARRRDRRLVLDEGVTVPQKRTDEWMELEMGEFINEEGEDGEVCFSLMETK
                                                                                                                                                                                                                                             codon_start=1
                                                                                                                                                                                                                                                                                                                                         note="contains EST(s): AU092429(C50563)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .2468
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                                                                                                                                                                                                                                                                                                         AK060823, AK098981
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/ COGOR STATE-1

/ COGOR STATE-1

/ product = "glutathione reductase"

/ protein _id= "BAD21653.1"

/ db _xref="Gl:47847860"

/ translation="MARKMIKDEEVEVANTDGGSYDYDLFVIGAGSGGVRGSRTSASF

/ translation="MARKMIKDEEVEVANTDGGSYDYDLFVIGAGSGGVRGSRTSASF

/ translation="MARKMIKDEEVEVANTDGGSYDYMIEGAGSLVDAHTVEVTKEDGSK

GRYTAKHILLENKTOEIVRLNGVYQRILGNSGVTMIEGAGSLVDAHTVEVTKEDGSK

GRYTAKHILLATGGSRAGRVNIEGKELAITSDEALSLEELFKRAVILGGGYIAVEFASI

WKGMGAHVDLFYRKELPLRGFDDEMRTVYVASNLEGRGIRLHPGTNLSELSKTADGIKV

VTDKGEEIIADVVLFATGRTPHSQCRLMLEAAGVEVDNIGAIKVDDYSETSVPYIWAVG

DVTNRINLTEVALMEATCFSKTVFGGQPTKEDYRDVFCAVFSIPFLSVVGLSEQQALE

EAKSDVLVYTSSENDMKNSISKRGEKTVMKLVVDSETDKVLGASMCGFDAPEIIQGMA

VALKCGATKATFDSTVGIHPSAAEEFVTMRTLTRRVSPSSKFKTNL"

29382)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           non-coding transcript probably inactive due to including stop codon(s) in CDS" join(16132 . 16272,16375 . 16439,16593 . 16662,16996 . 17 16165 . 17388,18290 . 18363,18462 . 18545,19079 . 19166, 19260 . 19341,19675 . 19748,19971 . 20078,20180 . 20244, 20814 . 20927,21141 . 21240,21337 . 21390,21469 . 21564) /gene="OJI293 EO44-1" /note="contains EST(s): D22281(C10676),AU102120(C10676) contains full-length cDNA(s): AK100446,AK058270"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15858 . 20860

/gene="OJ1293_E04.4-2"

/gene="OJ1293_E04.4-2"

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15858 . 20860
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16996. .17067,17165. .17368,18290. .18363,18462. .18545,
19079. .19166,19260. .19341,19675. .19748,19971. .20078,
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                                                                                                                                                                                                                                                         GTCATTACTTCACTGGAAAAGGGATATTTGTTAATTGTGTGATGGTTTGGGACTGTTTCCT 65780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProGlyPheAlaSerThrGlnLeuArgAlaTrpSerIleLeuAspCysProTyrThrPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGAGGCGATGGCGCGCGGATTTC----GACTACCGGAAGCTCTCGGGGATAATAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SerValThrAlaSerPheThrValIleAlaValPhePheLeuIleCysGlyGlyArgThr
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                                                                                                                                                             GTAAGGCGTCATACGGCTTAATTGGGTGAGGTTGTTACAGAAGCATTCAATCTGTGCAAT 65720
                                                                                                                                                                                                                                                                                                                                                     CGGTTGTGTGTACTACGTAACCATGCTAAAACTAGTGACACGTTCAGTTAGAAGAGGTTT 65840
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/gene="0J1293_E04.7"
35504. .35704
/gene="0J1293_E04.7"
/note="hypothetical O
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AYNLSGMGCSAGLVGVDLARRVMLTRRRTMALVLTSBSCAPNWTGTDXSMMLGNCLF
RCGGAAALLTNUDPAFRSRAKMELRCLVRAHIGAHDDAHAAVHREDADGRLKGVSLGA
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HFCLHPGGTAVIEAVRKSLGLDSYDVEPARMALHRWGNTSASSLWYVLSYMEAKRRLN
AGDRVLMVTFGSGFKCNSSYWVVTKDLADAGAWEDCIHDYPPANLVNPYMEKFGWVND
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64639 TACAATACTTGATAATGACACGGCGATATGTCGGAAATTCATTGTTGCATGCGGAAAGAT 64580  176	175 175	4/59 CANGCAAGCTGAAAATTGATAAATTTTTTTTTTGCGGGGGAAAATTGATAAGCTTTTACTTAC	4819 TCACGCAIAACTAAGTAGTACTAGTATCAGAAATACAAAAGTTAGCATTAGCATTAGCATTAGAAGTATAGAAGTATAGAAGTATAGAAGTATAGAAGTATAGAAGTATAGAAGTAGAAGA	48/9 CITCHAANIGIAICAACCAGAAHAHACICACLIIGIIIACCIICCAIACCAGACCAGAAHAHACII		175	169 uTyrPheH18Ly8LeuLy8	:::		129 uSerThrValTrpLyeGluTrpLeuLysTrpCysValGluPheGlyIleGluAlaAsnAl 149	65179 AGCCATAAAAAAAATCTTTCTTACTAATTTGGTTTTATTGGCCAAGTTTTCAGGTCCTCT 65120	ATGTTCATCGGTAAGCTGTAGAATTCCCCCATCTCGTTCCTCAAAGAATAAAA	126	126 126 65299 GAGTTAATAATGGATATTGCCATGAGAATAATAGCATTAGCTAGGTTACATTGCAAATTC 65240	126	126 5419	126	ArgProAspSerGlyLeuSerAlaileThrGluLeuAspProGlyTyrileThr 	65659 CATTITICATACTIGCGACTITAATCGGGTTCATGGTGCAGCTCTTATCTGCTGCTGAATTGC 65600  89 TrpPheLysCysMetValLeuaspProTyrAsnGlnThrAspHisProGluCysLysSer 108
Qy 320 lelleAsnIleGluIleProSerThr-SerVal	QY 300 rgValTyrHisCysAspGluGluGluTyrGlnSerLysTyrSerGlyTrpProThrAsnI 320                :::   :::	QY 283 SPASNThrSerTrpThrHisPheSerGlyGlyAlaAlaLysLysAspLysA 300	OY 263 euSerAsnSerPheAlaSerSerLeuTrpLeuMetProPheSerLysAsnCysLysGlyA 283 ::    :::	QY 258 263 263 263 Db 63739 TATATTGTCTTATGCATCTAAAATTGCTTTTATTGTTTTCAGGGAACAGCACGATTGA 63680	QY 257 257  Db 63799 GTTGAATCTGTACTTAGCTATATATTGCCAAAAATTGTTACATTATATGCCATCTTATAAT 63740	63859 CAGTTAGGGAGGTTGTTTTGGTGCATGTATAAATTCTCTACCTTCGAGTGATACACATGT	Db 63919 ACTTCTCATAGCCGATTCGCACGGCCAGGTTGTGTGTGCCACAACCATGCTAGTTTTAGAGT 63860  QY 257 257	Ob 63979 CTTCTACACGTGCAAGGGAACCTTTTAGTACTGTTGGAGTCTTGGAGACCAAAAAAAA	257	64039 TT	Db 64099 GTCCAATACTGAATAGTTTTTATTTCCTTTTTGGATTCACTAGGTTTTTGTGGTGATTCTT 64040	257	Qy 257	64219 GCCTTTATGAATTATATATTTTTCAATAATGTGTCCTCTGCCCCTCAGGAGGCTATATTTTC	AGCAGTTAAAGCTGCTCTTTCTGGAGCAACATTTGGTCTTCCAGTCAGCGAGGTCA	232 64339 GTT	224 isileHisalaTyxPheAlaVal	cgcrcccaagcarracarccgarggcrrgacgaac	

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AUTHORS 2 (bases 1 to 147123)  REFERENCE 2 (bases 1 to 147123)  AUTHORS Sasaki, T., Matsumoto, T. and Katayose, Y.  TITLE Direct Submitsed (05-SEP-2002) Takuji Sasaki, National Institute of Submitted (05-SEP-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan  (E-mail:teasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,  Tel:81-298-38-7441, Fax:81-298-38-7468)  COMMENT Genes were predicted from the integrated results of the following: Genes were predicted from the integrated results of the following: (http://www.softberry.com/), GeneMark.hmm  (http://paal.biology.gatech.edu/GeneMark/), GlimmerM  (http://paal.biology.gatech.edu/GeneMark/), RiceHMM  (http://rgp.dna.affrc.go.jp/RiceHMM/), SplicePredictor  (http://bioinformatics.iastate.edu/cgi-bin/sp.cgi), sim4	SOURCE Oryza sativa (japonica cultivar-group) SOURCE ORGANISM Oryza sativa (japonica cultivar-group) Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatcophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.  REFERENCE 1 AUTHORS Sasaki,T., Matsumoto,T. and Katayose,Y. TITLE Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2, BAC Clone:OSJNBa0053L11		61953 AACAAAGATGAATGTCGACCACCATGTAGGCCAGGCATACTCCCAAAGATGACAAGATGTCGACCACCACGATGTAGGCCAGGCATACTCCCCAAAGATGACAACGATGTAGACCACCATGTAGACCAATGTAAAGATGCTTAGAAGATGCTGAAGAGCATTCCGGGATGGAGAACCTACCT	62073 TTGTTGTGGCTAATAGAATTATTGACTGTTTCCTTGTAGCATATCACAATGTTAATGTGC  487	470 rTrpCysLysAsnTrpLeuGlyProLysVallasnIleThrMetAlaPro	62373 462 62313 463

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(http://www.tigr.org/software/glimmerm/), BLASTN and BLASTX. The genomic sequence was searched against NCBI NonRedundant Protein database, nr (ftp://ncbi.nlm.nih.gov/blast/db) and the cNNA sequence database at RGP or DDBJ. Protein homologies of the coding regions were searched against NCBI NonRedundant Protein database with BLASTY. ESTs represent the identified cDNA sequences using BLASTN with the corresponding DBJ accession no. and RGP clone ID. Full-length cDNAs represent the identified cDNA sequences using BLASTN with the corresponding DBJ accession no.

A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-' and '-like protein'. A gene without significant homology to any protein but with full-length cDNA or EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted by a single gene prediction programs is classified as a 'hypothetical' protein according to IRGSP standard. A gene predicted by a single gene prediction program is also classified as a miscellaneous feature of the sequence.

The crientarion of the sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The orientation of the sequence is from -21M13 to M13rev of the clone. This sequence of OSJNBa0053L11 clone has an overlap with P0016F11 (DBD; AP005303) clone at 5' end and with OJ1293_E04 (DBD: AP004120) at 3' end. Detailed information on overlap and assembly quality together with annotation of this entry is available at http://rgp.dna.affrc.go.jp/GenomeSeq.html.
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join(4586. 4894,4982. 5164,5251. 5600,6156. 6333)
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contains full-length cDNA(s): AK119257,AK063935"
                                                                                                                                                                                                                                                              /gene="OSJNBa0053111.3"
/gene="Supported by full-length cDNA(s): AK119257"
/gin(4438. .4894,4982. .5164,5251. .5600,6156. .6725)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       join(<2264. .2293,2852. .>3226)
/gene="OSJNBa0053L11.2"
/notee "start and end point are not identified"
join(2264. .2293,2852. .3226)
/gene="OSJNBa0053L11.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                predicted by GENSCAN this category is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="OSJNBa0053L11.2"
join(<2264. .2293,2852.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPPRRDTANPSTRHGGQTAAATRWPPLGSTCG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /trānblation="machgdayvsrrrgtnsaratespprrqasasargsiasaatrd
sanaeglrplwlsasalshgsvtsaitrnsyavnvatsrgspslppratppaargyva
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/protein_id="BAD22377.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           join(210. .282,431. .528,603./gene="OSJNBa0053L11.1"
/note="hypothetical ORF
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/product="putative cinnamoyl CoA reductase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             xref="taxon:39947"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             category is not included in IRGSP standard"
                                                                                                       start=1
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misc_feature
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Pnlvpvalegtrnwkkaadmgvrkvvftssygavhemprnspdavldeschhvvryltig
Qrediycyakwaektatebasrricolavvvpcvtvgpilqpsvnfschhvvryltig
Aaatypnavaayadvedvaaahvlvyehhgargrylcigtvihraellrmlkelfpqy
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rpdldvwrlvalasdgggwtgvavavavamamvadggggsdggyrrcylwrrwlka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="start and end point are not identified" complement(join(7826 . 8214,8309 . 8435)) /gene="OSJNBa0053L11.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (join (<7826. .8214,8309./gene="OSJNBa0053L11.4"
                         AHLRCRRLVFPLTRLTYYAAISGHLRFHRRPDSSPPTGVFIVIDGRLCSHIGHFCHHQ
GEYYKAKNGSVRTSPPARLDRRRLVFPPARLAFMPPLLGVYVFTDRLAFAAADMCFRL
HGWPLCRRCWASTSSPTGRLVRRRLVLFPAAAVVGRLRLHRPAASSAADMCFR
LHGWPIMPPLLGVYVFTDRLAFAAADMCFRLHGWPIMPPLLGVYVFTDRPPRPPFTGA
SACTAGILCRRCWASTSSPTGLPSPPTGVSACTAGLYATVVGRLRLHRLACLRRCRL
VFPPBRRLAFWPPLLGVYVFTDRLAFAAADMCFRLHGWPLCRRCWASTSSPTGLPSPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="OSJNBa0053L11.6" complement (join(12759.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9814. .11214
/gene="OSJNBa0053L11.5"
/gin(<9814. .10128,10328. .10525,10605. .10954,11058. .>11214)
/gin(<9814. .10128,10328. .10525,10605. .10954,11058. .>11214)
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                                                                                                                                                                                                                                   RRRLYPPPTRVAYYAAAVGRLRLHRRPAFAAADWCFRLHGWPIMPPLLGVYDFTAGLS
PSPPSGASAYTAGLLCRRCWASTTSPPAYLRRRRVVPPPTRLAYYAAAVGRLRLHRRP
ASVAAEWCLRLHGWPIMPPLLGVYDFTAGLPPSPPSGASAYTAGLLCRRCWMSTSSLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         this category is not included in IRGSP 15304. .18533 /gene="OSUNBA0053L11.7"
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VANYLTGAKKSYPNAVAAYVDVRDVARAHALVYERHDARGRYLCIGAVLHRAQLLQML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /t.Tanslation="MSSISNDNNGDQKRQQQQQLVCVTGAGGFIGSWVVRELLLRGYR
VRATVRDPADRKNAHLLALEGAHERLSLRRADVLDFAGLLAAFAGCHGVFHVACPLSN
RDPELMAVAVDGTRNVMNAAADMGVRRVVFTSSYGAVHMNPNRSPDAVLDESCNSDPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="putative cinnamoyl CoA reductase"
/protein_id="BAD22380.1"
/db_xref="GI:47848528"
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/note="start and end point are not identified"
join(15304...16325,17024...18533)
/gene="oSJNBa0053Lll.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     predicted by GENSCAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="OSJNBa0053L11.6"
/note="hypothetical ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MDLFPQYTIASKCDDKGKPMVKPYEFSNQRLKDLGLEFTPLRKSLYDAVMCMQRNGHL
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TGVSACTAGLLCRRCWASTSSPTGRLVRRRLVLPPARLAYYAAVVGRIRLHRPACLRR
                                                                                                                                                                                                                                                                                                                                                   PTGVLAYTVGWSHHRSWASTSSPTGWPSPPPTGVSAYTVGLLCHRCWASTTSPPACLR
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/db xref="G1:47848529"
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127937 GTCATTACTTCACTGGAAAAGGGATATTTGTTAATTGTGATGGTTGGGACTGTTTCCT	OV 81	81	Db 128057 ATCTGCTTGATTTGAGTGACCATCTAGTTATAGGTTTTTGGAAGTGTTTTTAGGACTAAAT 127998	Qy 81 81	Db 128117 TTGATGGATTAAAGTAATTTTGCAATGGCCCATCAGGCAGATGCGTGTGTGCGACTGCAC 128058	Qy 81 81	128177 TGGATAATATATGTGCTTTTGTTCTTTTATTAGGATTCGTTGGTCTGTTCTTGTGAGGCA	Db 128237 CGTTCCGTACTGTCCTGATATTCAGAAAGCTACTTTTGCTAGTAACTGTTGTTGTTGTTC 128178 OV 81	81	Qy 67 LeuAspPheAsnProLeuAspLeuValTrpLeuAspThrThrLys	Qy 47 ProG.yPneA.aserinrG.inLeuArgAlairpSerlieLeuAspcy8ProGyrinrPro 66	128411 GGAGGCGATGGCGGCGGGATTTCGACTACCGGAAGCTCTCGGGGATAATAATC 1	27 AlaValGluAspGluThrGluPheHisGlyAspTyrSerLysLeuSerGlyIleIleIle 46	Db 128471 TCGGTGGCGGTGGCGGTGGCGGCGGCGGTGGCGGCGGCGG	7 ServalThrAlaSerPheThrVal	91 (1-	Match: 50.03% Indels: 15 Gaps:		No.: 1.05e-115 Length:	•		c_feature (	KDVVVGEVVKLAK"  gene complement (join (2195922112, 2214922168))	/protein_ig="pauzzss.i" /db_xrefr="Gi:47948530" /translation="MEVEKEPVGNSQICVEGVQVEILNIGESLVVVKYHGIACRDVEVH	/codon_start=1 /product="hypothetical protein" /protein = 14, "pannongo" 1 "	/gene="0SJNBA0053L11.8" /note="predicted by FGENESH etc."	/gener="GoodwadowsJalla". /note="start and end point are not identified"  complement{foin(1899419134.1978619818)}	/gene="0SJNB80053111.8" mRNA complement(join1899419134,19786>19818))	FAAADWCFRLHGWPIMLPLLGVYVFTGRPPHPPLTDVTASTAGLL" gene complement(1899419818)
Qy Db	Qy	μ		망 왕	_		u	Q	Qy 12	L	Db 12	γ	Db 12	0 15		Db 12		Db 12	γ	ם מם	Ş	Оу Дъ 12	Db 12	ργ	Db 12		Db 12	); 	
26857 CATGCAAGCTGAAATTGATAATTTTTTTTGCGGGGGAAATTGATAAGCTTTTACTTGCTT 126798 175 175	175 175	26917 TCACGCATAACTAAGTAGTACTAGTATCAGAAATACAAAGGTTTGGTTGCCTTTGGTGTG 126858	175	1/5	TCACTGCCCATTGGCTTTCGATATTTGATGTTALTACTAATAATTGGTGTAAAAAAA	175	GTACTTCCATAAATTAAAGTTTGTAACACTTCACTTCATATCACATAGCAATCAAT	uTyrPheHisLysLeuLys 175	149 alleValAlaValProTyrAspTrpArgLeuSerProThrLysLeuGluGluArgAspLe 169     :::	TTCTTCAGTGTGGAAAGAATGGGTCAAATGGTGTGTAGAATTTGGTATTGAAGCTAATGC	7277	127GlyProLe 129	7337 ATGTTCATCGGTAAGCTGTAGAATTCCCCCATCTCGTTCCTCAAAGAATAAAAAAATGATT	2/39/ GAGTTAATAATIGAATATTIGCCATGAGAATAATAAGCATTAGCTAGGTTACATTGCAAATTC 12/330	126 126	7457 TGGAAAAAAAACCATUGATGGCAAGTGAGAGATAAAATITGACATCAAGCTIIIGI	126	7517 ATGCTGCACGATTCATCAGCAATGTGATAGATTGTGATTTATGCTTCAACTCCCATGCAA	126 126	27577 TTATATGCCTCGCTTAATTCTCCTTGGTATTGATTGGATTATTGAATTTTGAGTACAAAT 127518	126 126	109 ArgProAspSerGlyLeuserAlaileInrGluLeuAspProGlyTyrIleInr 126 	7697 TGGCTCAAATGCATGCTGCTCGACCCTTACAACCAGACGGATCATCCAGAGTGCAAGTCA	89 TrpPheLysCysMetValLeuAspProTyrAsnGlnThrAspHisProGluCysLysSer	27757 CATTITCATACTTGCGACTTAATCGGGTTCATGGTGCAGCTCTTATCTGCTGTCAATTGC 127698	82	7817 GAACAGGCTGTAACGATTATATTTGTTACATGTAGGGGGTCATATTTAAGTATTATCTTT	2/8// GIAAGGUGICHIACGGCIIAHIIGGGIGNGGIIGIIACHANNACHIICANACHGIGCNNI 12/010	81

283 spAsnThrSerTrpThrHisPheSerGlyGlyAlaAlaLysLysAspLysA 300	263 euSerAsnSerPheAlaSerSerLeuTrpLeuMetProPheSerLysAsnCysLysGlyA 283 ::    :::	258	257 257 Db 25897 GTTGAATCTGTACTTAGCTATATTTGCCAAAATTGTTACATTATATGCCATCTTATAAT 125838 Qy	257 257  259 CAGTTAGGGAGGTTGTTTGGTGCATGTATAAATTCTCTACCTTCGAGTGATACACATGT 125898	ACTTCTCATAGCCGATTCGCACGGCCAGGTTGTGTGTGCCACAACCATGCTAGTTTTAGAGT 125958	257 257   Qy 257 257   Db	257 257  257 TTGCCCCTTGTTCTTGTCCCTGCCCTTTCTGAGAGTACTGTTCTGGTAACCTCTCAGCC 126078	257 257 Db 126197 GTCCAATACTGAATAGTTTTTATTTCCTTTTTGGATTCACTAGGTTTTTGTGGTGATTCTT 126138	257 257  Db  126257 TGATATTTATACATTTTTCCTCCAACATTGTTAGTGTTGAATTTAAGTATGTTGTTGGTT 126198  Qy	GCCTTTATGAATTATATATTTTTCAATAATGTGTCCTCTGCCCTCAGGAGGCTATATTTC	239 alGluAlaIIoLysSerThrLeuSerGJyValThrPhGJyLeuPrOValSerGIU 25/       :::  :::	GTTATTTGTTAGTGTCATGCCATTTTTCCTTGCTTTCAGGTGCACCTCTTCTTGGTTCTA 126378	224 islleHisAlaTyrPheAlaVal	heLeuGluTrpLeuArgLeuGluIleAlaProLysHisTyrLeuLysTrpLeuAspGlnH 224            :::   Db TTCTGGAATGGTTGAAACTAGAAATCGCTCCCAAGCATTACATCCGATGGCTTGACGAAC 126498	euArgGlyGlyProSerIleValPheAlaHisSerMetGlyAsnAsnValPheArgTyrP 204	AGTATTTTGGTGCTCATAGTCCTTTTAACTGCAGGTTAACTTTTGAAACTGCATTGAAAC 126618	TACAATACTTGATAATGACACGGCGATATGTCGGAAATTCATTGTTGCATGCGGAAAGAT 126678
124651 TAATTTGATTGAATGAAGATCCTAGTAAGTTGCACTGGTTTCTAATGGTAATTACCACAG	124711 T	b 124771 TCAAATTATCCATTATCTGTCTTTATGTATGTCTGCTTCTAGTGTAGTTTCCTGGAACAG 124712		124891 A	416	415 VAL	125070 TGGGAGAGCCCCCAATAAAGAATGTGTTCTGCATATATGGGCTTGATTCAAAGACTGAG	125130 1	125190 T 383 -	D 125250 AATTCTCAGTTTCACATACATATTTATCTTCAAAGTAAACCACCAACTTACATGTTTTTA 125191	125309 CAGCTTGAGAAGTG-AGTTTGCAATTTTGTATGCGCCAGTGCTACTTTGTAAATTGT 125251 9 382 382	125369 378		125489 T	125549 ATCTATGATTAAGATTTTGCTTCCACTGAGCAGGTCTACCTTTTCTTTC	125609 TTGTCAGCATCGAGGTTCCTACAGTTCGAGGTTCTTGTTGAAATTTCTTCCCAGCTTTA	125658 -

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Published Only in Database (2002)
2 (bases 1 to 158971)
Sasaki, T., Matsumoto, T. and Yamamoto, K.

Direct Submission
Submitted (20-MAR-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan
                                                                                          Oryza sativa nipponbare(GA3) genomic DNA, clone:00511E12
                                                                                                                                               AP004882.1 GI:19698302
HTG; HTGS PHASE2.
Oryza satīva (japonica cultivar-group)
Oryza satīva (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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*** SEQUENCING IN PROGRESS ***.
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/cultivar="Nipponbare"
/db xref="taxon:39947"
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1483.50
29.50%
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Matches:
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(E-mail:tsasski@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Pax:81-298-38-7468)
NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved. ocation/Qualifiers

(japonica cultivar-group)"

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59705	TGGATAATATATGTGCTTTTGTTCTTTTATTAGGATTCGTTGGTCTGTTCTTGTGAGGCA 59705	59764	8
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59885	ProGlyPheAlaSerThrGlnLeuArgAlaTrpSerIleLeuAspCyeProTyrThrPro	47 59944	8 8
46 59945	AlaValGluAapGluThrGluPheHisGlyAspTyrSerLysLeuSerGlyIleIleIle	27 59998	8 8
26 59999	SerValThrAlaSerPheThrValIleAlaValPhePheLeuIleCysGlyGlyArgThr:	60058	8 8

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Qy       257	257 57904 GC 257 57844 TC 257 57784 GT 57784 GT	Oy 204 heLeuGluTrpLeuArgLeuGluIleAlaProLysHisTyrLeuLysTrpLeuAspGlnH 224	Db 58384 CTTTTCATTTTTTATGACATCCTTTCACTTGAAATTAAAAGTTGTTTCTCAAGTTTA 58325  Qy 175

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	446 446
AUTHORS Asamizu,E., Kato TITLE Structural Analy	56358 TCAAATTATCCATTATCTGTCTTTATGTATGTCTGCTTCTAGTGTAGTTTCCTGGAACAG 56299
rosids; eurosids Lotus.	446 446
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Db 55698 CTTTCCTGCTTTG	TATGCTTATGGAAGTAAATATGTGTGATTTGATTAAATTGTATCTAATACCCCCCACATT
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Db 55758 TTGTTGTGGCTAA	382
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55	378 GlnLeuLysLysLeu 382
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Db 55998 AGCCCAACAATTC	337
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Db 56178 ATAATAGCTTTTCC	300 rgValTyrHisCysAspGluGluGluTyrGlnSerLysTyrSerGlyTrpProThrAsnI 320
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APO06356
APO06356
Lotus corniculatus var. japonicus genomic DNA, chromosome 6, clone:Lj706108, TM0082b, complete sequence.
APO06356.1 GI:31580987
HTG.
Lotus corniculatus var. japonicus (Lotus japonicus)
Lotus corniculatus var. japonicus (Lotus japonicus)
Lotus corniculatus var. japonicus
Eukaryota; Viridiplantus; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids ; Fabales; Fabaceae; Papilionoideae; Lotus.
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Structural Analysis of a Lotus japonicus Genome. IV. Sequence Features and Mapping of seventy-three TAC clones which cover the Patures and Mapping of seventy-three TAC clones which cover the Patures and Mapping of seventy-three TAC clones which cover the NA Res. (2003) In press
2 (bases 1 to 93398)
Sato, S.
Direct Submission
Submitted (07-MAY-2003) Shusei Sato, Kazusa DNA Research Institute, Submitted (07-MAY-2003) Shusei Sato, Kazusa DNA Research Institute, Sator, S.

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Oy 83LeuSerAlaValAsnCyeTrpPheLysCysMetValLeuAspProTyr 98	Db 33803 TTCTATTGAATTTGTGAACCTAGCTTTAGCATCCATGAACACCTTATGAGGATTTGGTTT 33744	Оу 82 82	Db 33863 CTACTATAAGCTATTTTTTTGACTTATTTGAATGAGTTTATGAATTTTATCCTAATACAC 33804	82	33923 ACTGTTTCCTGAACAGGTGACAGAGTCTGTCAAAGAATAAAAAGAAAG	82	CY 82	34043 AAGGTTTTTTATAGCTTATTTTAGTAACTTTTTTCTGAAGTTAGTT	82	Db 34103 TGATTGTTCATAGTATAACTATAAGTACATGCTTGATTAAATTTATGAAGAGCTTAGGAT 34044	Qy 82 82	Db 34163 ACGTTTCCATGCCAATCCTTTCTGTTTCATTCTCTAGGTGATGATTTTTTCTTGA 34104	Qy 82 82	Db 34222 CCTTACTCTCCTCTCGATTTCAACCCTCTCGATTTGGTCTGGTTGGACACCACCAAAGT- 34164	eAsnProLeuAspLeuValTrpLeuAspThrThrLysLeu 82	TCGATTCTTGACTGC 3	43 GlyIleIleIleProGlyPheAlaSerThrGlnLeuArgAlaTrpSerIleLeuAspCys 62	TACTCGAAGCTCTCC 3	GlyGlyArgThrAlaValGluAspGluThrGluPheHisGlyAspTyrSerLysLeuSer 42	CAACAAACCGCTGCTATGCTTCCTAACCGTC	Qy 3 AlaAsnSerLysSerValThrAlaSerPheThrValIleAlaValPhePheLeuIleCys 22	US-09-651-651-5 (1-546) x AP006356 (1-93398)	15.12* MISMACCHES: 30.86* Indels: 15 Gaps:	ont Similarity: 17.05%	вупонущ: посна јарописна	/Clone lib="Lj: library" /note="TM0082b, a part of TAC clone:TM0082. symonym. Loting laponicus"	/chromosome="6" /clone="LjT06I08" /clone="LjT06I08"	/mol type="genomic DNA" /variety="japonicus" /db_xref="taxon:34305"	source 1. 93398 /organism="Lotus corniculatus var. japonicus"	Chiba 292-0818, Japan (B-mail:ssatc@kazusa.cr.jp, URL:http://www.kazusa.cr.jp/, Tel:81-438-52-3935(ex.2337), Fax:81-438-52-3934)	303 0010 13535
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257 257	31585 TTGATCCAATATTACCTTGTCTAATGCTGTTAATGGCGGATGGCAGACCATGGCTAGAGC 31	257	5 GACTATAAACTTGGAAAAGATAACAGGATAAACACACTTGAAATCTGCATCAAGGAAATG 31	257 257	31705 GTTTTATTGGGTTTGGATTTGAGTTGTCGAACATGCAGTTATAATAGGTGATTCCAAGTAG 31	257	Ob 31765 CTTTCTGAAGGTCTGTATTCCTTCAAGAAGTCTTTAAAGAACTTTACTGAGTTACTTGCTTTCT 31706	257	Oy 257 257	31885 GCCTAGGACATATTGAATTCACACAAACCCACACAGAGTTGAGTAATTTGATTTAAA	257	31945 AACCAATTAAAGGTTAAATTATAAAAAAAAACTTATAATTATTTTGAATGGCCCAAGCTT	257	32005 CTGGTACTCTCTCTTCTTCAGCAGAACCTGGAAATTCTTCTATTTGTTCCAGACTTTA	257 257	32065 TTAAGTACTTCTTGCTTCATAAATTCAGTAATATTGTATTCTGATATGACACATAATGTA	257	32125 AAATTATAGGTCTCTAATTCTTTCAGATATTGCCAAATTCACAAAGTTTTTTTT	257	32185 TAGATTTTCTTTTCGGTTTGCCTTTTTATCTGACATTTATCTAGGTTTACTTGCTGTACA	257 257	32245 ACTCTCTGGTTTCACATTTGGTCTTCCTATATCTGAGGTGAACTTTTAATATTTTGTAACT	245 rLeuSerGlyValThrPheGlyLeuProValSerGlu	Db 32305 CTTTTGATCGGTTGTCTCAGGAGCTCCCCTTTTGGGTGCAACTGAAACCGTCGAAGCAAC 32246	Qy 232GlyAlaProLeuGlySerValGluAlaIleLysSerTh 245	Db 32365 TGCATTTATTACATTTTATCAGTATTGCTGATTAAGTGATATATTGGTATGCTGATTTTC 32306	Qy 231 231	Db 32424 TTTCGAATGGCTGGATCAACATATTCACGCATATTTTGCTGT-TGGTATGTTTACATATG 32366	Qy 217 rLeuLysTrpLeuAspGlnHisIleHisAlaTyrPheAlaVal 231	Db 32484 TAATCACGTTTTTCGTTATTTCTTGGAGTTGGAAGCTAGAGATAGCACCAAAACATTA 32425	Qy 197 yAsnAsnValPheArgTyrPheLeuGluTrpLeuArgLeuGluIleAlaProLysHisTy 217	Db 32544 ATTTGAAACTGCTTATAAACTTCGAGGTGGCCCCTCTTTAGTTTTTGCCCATTGATTG	Qy 177 rPheGluThrAlaLeuLysLeuArgGlyGlyProSerTleValPheAlaHisSerMetGl 197	Oy 1/6
Qy 257 257	Db 30505 CTCTTACAATTATTCATGCATAGTAGAAAGTACTTATCTGAAGAGCTAGCT	Qy 257 257	Db 30565 CCATACTTCTCGTTATATATTACATGCTTCTAAGTCGTTTTCTTATTGACGACATGAAAC 30506	Qy 257 257	Db 30625 TTTTTGTATTGTTCTTCAATTACAATGCTGAACTGTTGAAATACATCTTTTGCTGGAATT 30566	Qy 257 257	Db 30685 ATTTCCATTAAAACCTATTCTTTATAGTTTTTTAAGAAAATAATAAAATCCCTTGAGA 30626	Qy 257 257	Db 30745 CAAATGAAAGAGAGAGAAAAAAAGGACTTCGAACTTTCGAAACCTTACTGACATATATT 30686	Qy 257 257	Db 30805 AAATTGGAGCATTTTACTATAGAATAATTTCATGTAAGGGTAAAATTTCTGAAAGCTGCT 30746	Qy 257 257	Db 30865 GAGAACCGAGAAGGAAATTTTCATCTTGATGAAGATGCTCAATATCATCTAGGGCATGGG 30806	Qy 257 257	Db 30925 AATATTTTCAATTTTAAATTTAAACAGAGGTTAAATTCAAAGAAACAACTTGCAGTAAGGG 30866	Qy 257 257	Db 30985 TTGAAGTGGGCTTAATGTCCTAGATTTTAGGATTAGAGTTTGAATACAATTTGGAGAAAG 30926	Qy 257 257	Db 31045 CCTACTCATGCATTAGAAGTGGGCTTAATGTCCCATATTTGGAAAATCACTTGCTCATGC 30986	Qy 257 257	Db 31105 TGTTTCTAAATATTCACCTATATCATGGCATCATGATATGGGGGGCAGATTTGGAACATTG 31046	Qy 257 257	31	257	31225 TTTTGGTCTAACAGCATCATACAACTTCCTTGTCATTATTCATTAGTGGTCTTTAATCAT	257	TATTTAATCATTAACTTTGACACCCCAGGCATTGCTTGAGCTGCTTGAATAATTCAGCTGT	257	31345 CATCTCTCTGTGCTGTTGTCTTAACAGGAATAGCACCCACTTCATAACTTTTTAATATCT	257	CACAGCTTAACAGTCATATAACCCCACTTACAATGATTGTGACTTTAATAGGATGCATGAA	Db 31465 ATGGCGGAGAGCCAAAAACCCATCATGAGATTCGACGCGCCATGGCAAAAAATATTTGATAA 31400	257	31525 CAAACCCTGCTATATTGGATTGGACAAATAATGGTGGCGGATTATGGCTTGATATCGGCC

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27271	TTAGGAAGGCATGATATATTGATCGTCCTACACAATTTTATGGAATTGCAATACATTAAA 2	27330
162	4	462
27331	`D'	27390
162	lyAspGlu 4	460
27391	GACCC	27450
160	rgSerGlyThrValValAspGlyAsnAlaGlyProIleTh	446
27451	TTGCAAATTAATGTTAGTATTGTTCATTTTTTGGATATCCTATTTTAACATGTTACGGTG 2	27510
145	4	445
27511	CCTTTTTTTTGGGATGGGAGTTGAGGGATGGTTACTTGGTTAAAATATTTGACATTCATT	27570
145	4	445
27571	GTTTTGGCATAACCAGTTCGTATAAGAGGAAAATCTAGACTAGCTTTTGTTAGTCATCAT 2	27630
145	4	445
27631	TAATAATGACATCTTTCTTTCAAATTGTTGACCAACAACCTCCTTGGTCATGGTGCTGCC 2	27690
145	4	445
27691	GCTGCTAGCTCCTCTTTTGCTCTGTCTTGCAAAGTATTGGTATCTTGTGTATCATCTCAT 2	27750
145	4	445
27751	TGATATCTCTCTTTATTAATTGCTCTTGTTGGTTGAACTTGGGTGCATAGTATTTTGAC 2	27810
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7811	CTATGTCCTCTTTTTTTAGAGGGGGGGGGGGGGGGGGGTTACCTTCCAGGATTAAAGGA 2	27870
145	4	445
27871	CTGCTGTTCCAGAAGAATACCTTCTCTTTATGCATTTTCAAATTCTTCTCTATTCTTTTT 2	27930
45	4	445
27931	TTTTTATTTTGTACTTCATGGATTATGTTTCATTACATAAAGTTACCACAATACTTGTCG 2	27990
145	4	445
27991	ATCAGTTGTAAATGGAATGAAAATTCTATTATCATCAGTTTGAAGGATCTCTCTC	28050
45	4	445
8051	ATTTCTATGGCGGAGTGAAATCAAAGAGAGAGAAAGATAGAAAGATCTAAGTCTACTGTG 2	28110
145	4	445
œ	TTTTTGTGATTAA 2	28170
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-Q2/G9n2 1/USPTO spool/US09651651/runat 18112005 101830 20237/app query.fasta 1.711
-DB=N Geneseq -QFMT=fastap -SUFETX=rng -MINMATCH=0.1 -LÖOPCL=0 -LÖOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
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## ALIGNMENTS

31-MAY-2001

(first entry)

AAS01082 standard; DNA; 1641

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Lecithin: Cholesterol acyltransferase-like; LCAT; sterol acyltransferase; acyl CoA: cholesterol acyltransferase-like; ACAT; plant oil; cooking oil; nutritional supplement; dairy product; food product; salad dressing; ds.
                                                                                                                                                                                      Arabidopsis thaliana sterol acyltransferase LCAT2 DNA.
 30-AUG-1999;
                   30-AUG-2000; 2000WO-US023863
                                       08-MAR-2001.
                                                          WO200116308-A2
                                                                                                                            Arabidopsis thaliana.
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                                                                                     /*tag=
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                                                                              product= "LCAT2"
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CC (AASO01081-AASO1104, AASO1311) and ACAT (acyl CoA:cholesterol
CC acyltransferase-like; AASO1311-AASO1319) are described. A yeast LCAT
CC acyltransferase-like; AASO1311-AASO1319) are described. A yeast LCAT
CC related open reading frame, LRO1 gene sequence (AASO1342), and a rat ACAT
CC (AASO1105) cDNA sequence are also described. The polynucleotides encoding
CC LCAT or ACAT are used to produce LCAT or ACAT polypeptides. They can also
be used in a recombinant construct to transform a host cell (preferably
CC of a plant) or a plant. The recombinant construct is used to increase or
CC decrease the sterol content of the host cell or plant. It can be used to
CC alter oil production of the cell or plant, preferably by increasing it.
CC The oil of the plant or the plant itself is used as a food product, or as
CC nutritional or dietary supplements, or in pharmaceutical compositions for
CC obstitute cooking oil, and dressings e.g. salad dressings, mayonnaise,
CC butter, cooking oil, and dressings e.g. salad dressings, mayonnaise,
CC cheese, processed meat, pasta, sauces, cereals, desserte, dips, chips,
CC baked goods, pastries, cookies, snack bars, confections, chocolates, and
CC provide a plant with tolerance to stress and insect damage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid encoding plant lecithin:cholesterol acyltransferase acyltransferase-like or acyl (coenzyme A) CoA:cholesterol acyltransferase-like polypeptides, for modifying the sterol content and oil production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence encodes for Arabidopsis thaliana lecithin:cholesterol acyltransferase-like 2 (LCAT2). Several
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RESULT
The present invention describes a nucleotide sequence (I) derived from a CC nucleotide sequence encoding an acyltransferase polypeptide comprising at C2 least one membrane-spanning region. (I) encodes an improved active membrane independent acyltransferase polypeptide in which at least one CC amino acid residue of the membrane-spanning region has been deleted and/or substituted as compared to the original acyltransferase CC polypeptide, where the encoded active membrane independent CC acyltransferase polypeptide can produce fatty acid esters and/or fatty CC acid thioesters such as triacylglycerols, diacylglycerols, carylated carbohydrates and acylated anno acids. Also described: (I) a CC acylated carbohydrates and acylated mino acids. Also described: (I) a CC acylated carbohydrates and acylated mino acids. Also described: (I) a CC which functions in a host, where the promoter region is operably linked to at least one promoter region which is operably linked to at least one non-cc translated region which functions in a host; (2) a vector comprising (II) (3) a host cell comprising (II) or the vector; (4) producing an comproved active membrane independent acyltransferase polypeptide,
                                                                                                                                                                                                                                                                                                                                                                        New nucleotide sequence encoding an improved acyltransferase polypeptide, useful for producing structured lipids or fat-soluble molecules, in removing undesirable fat or in modifying lipids in animal or plant raw
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20-JAN-2003; 2003SE-00000142.
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               PheArgTyrPheLeuGluTrpLeuArgLeuGluIleAlaProLy8HisTyrLeuLy8Trp
                                                                                                                               AlaLeuLysLeuArgGlyGlyProSerIleValPheAlaHisSerMetGlyAsnAsnVal
                                                                                                                                                                                      ProThrLysLeuGluGluArgAspLeuTyrPheHisLysLeuLysLeuThrPheGluThr
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Phospholipid:diacylglycerol acyltransferase enzymes in the biosynthetic pathway for triacylglycerol production and DNAs encoding them, useful for producing triacylglycerol, or for transforming any cell or organism to increase oil content.

WPI; 2000-665012/64.

Claim 6; Page 60-61; 97pp; English

The present invention describes an enzyme for catalysing (in an acyl-CoA-independent reaction) the transfer of fatty acids from phospholipids to diacylglycerol in the biosynthetic pathway for the production of triacylglycerol (TAG). The enzyme is designated as phospholipid:diacylglycerol acyltransferase (PDAT). The enzyme and the nucleotides encoding them are useful for producing TAG and/or TAG with uncommon fatty acids. The enzyme and the nucleotide are also useful for transforming any cell or organism in order to be expressed in this cell or organism and result in an altered, preferably increased oil content of this cell or organism. The present sequence represents the Arabidopsis thaliana PDAT genomic DNA

Sequence 3896 BP; 1042 Α, 725 Ç 769 <u>ი</u> 1360 Η; 0 ä

Alignment Scores:  1.33e-223  Pred. No.:  2332.00  Matches:  541  Score:  541  Percent Similarity:  41.58\$  Conservative:  78.65\$  Best Local Similarity:  78.65\$  Conservative:  78.65\$  Indels:  759  Best Local Similarity:  78.65\$  US-09-651-651-5 (1-546) x AAC64438 (1-3896)  US-09-651-651-5 (1-546) x AAC64438 (1-3896)  US-09-651-651-5 (1-546) x AAC64438 (1-3896)  Oy  1 MetGlyAlaAsnSerLysSerValThrAlaSerPheThrVallIteAlaValPhePheLeu  Oy  1 MetGlyAlaAsnSerLysSerValThrAlaSerPheThrVallIteAlaValPhePheLeu  Oy  2 IleCysGlyGlyArgThrAlaValGluAspGluThrGluPheHisGlyAspTyrSerLys  Db  6 ATTTGCGGTGGCCGAACTGCGGTGAAGTGAGACCGAGTTTCACCGCGACTACTCGAAG  Oy  41 LeuSerGlyIleIleIleProGlyPheAlaSerThrBlnLeuArgAlaTrpSerIleLeu  Db  12 CTATCGGGTATAATCATTCCGGGATTTGCGTCGACGTACTACGAGCTTCCTTT  Conservation Assable	,	· -		_	^	_	_	_	н	_	m		r۸	-	~
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                                                                        The present invention describes an enzyme for catalysing (in an acyl-Co independent reaction) the transfer of fatty acids from phospholipids to diacylglycerol in the biosynthetic pathway for the production of triacylglycerol (PAG). The enzyme is designated as phospholipid:diacylglycerol acyltransferase (PDAT). The enzyme and the nucleotides encoding them are useful for producing TAG and/or TAG with uncommon fatty acids. The enzyme and the nucleotide are also useful for transforming any cell or organism in order to be expressed in this cell or organism and result in an altered, preferably increased oil content this cell or organism. The present sequence represents the Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                               Phospholipid:diacylglycerol pathway for triacylglycerol producing triacylglycerol, cincrease oil content.
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AAS01096;

31-MAY-2001 (first entry)

Corn sterol acyltransferase LCAT EST sequence #3

Lecithin:cholesterol acyltransferase-like; LCAT; sterol acyltransferase; acyl CoA:cholesterol acyltransferase-like; ACAT; plant oil; cooking oil; nutritional supplement; dairy product; food product; salad dressing; corn; Arabidopsis thaliana; expressed sequence tag; EST; ss.

WO200116308-A2

08-MAR-2001.

30-AUG-2000; 2000WO-US023863

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Best Local Si
Query Match:
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RESULT 6
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CC acyltransferase polypeptide can produce fatty acid esters and/or fatty CC acid thioesters such as triacylglycerols, diacylglycerols, waxesters, CC monoacylglycerols, phospholipids, glycolipids, lysolipids, waxesters, CC acylated carbohydrates and acylated amino acids. Also described: (1) a CC nucleotide sequence molecule (II) comprising at least one promoter region CC which functions in a host, where the promoter region is operably linked to at least one non-CC translated region which functions in a host; (2) a vector comprising (II) (2); (3) a host cell comprising (II) or the vector; (4) producing an CC improved active membrane independent acyltransferase polypeptide, CC comprising providing the above host cell and a growth medium preparing a cell culture, culturing the host cell culture and harvesting the cell culture and recovering the improved active membrane independent acyltransferase polypeptide; (5) a polypeptide obtained by the method in CC (4), where the polypeptide at least is an improved active membrane comprising the above polypeptide; (6) an oligonucleotide specifically hybridising to (I) under stringent conditions; and (7) a kit comprising the above polypeptide are useful in producing structured comprising lipids present in animal and plant raw material. The present condifying lipids present in animal and plant raw material. The present conditions is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            least one membrane-spanning region. (I) encodes an improved active membrane independent acyltransferase polypeptide in which at least one amino acid residue of the membrane-spanning region has been deleted and/or substituted as compared to the original acyltransferase polypeptide, where the encoded active membrane independent
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29-MAY-2002; 2002US-0383889P
20-JAN-2003; 2003SE-00000142
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phospholipid; glycolipid; lysolipid; waxester; acylated carbohydrate;
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  Renz A,
Lazarus
                      WPI; 2004-737701/72.
P-PSDB; ADT99410.
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17-OCT-2003; 2003DE-01048996.
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                                                                                                                                                                                                                                                                                                                                               WO2004087902-A2
                                                                                                                                                 (UYBR-) UNIV BRISTOL
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                                                                                Bauer J,
s CM, Qi B,
                                                                                  Frentzen M,
Abbadi A,
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LCAT; lecithin-cholesterol acyltransferase; gene; ss;
polyunsaturated fatty acid; PUFA; transgenic; acyltransferase;
lipid metabolism; animal food; human food; cosmetic; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fusarium lecithin-cholesterol acyltransferase (LCAT) cDNA Seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TyrPheAla-----ProSerGlyLysProTyrProAspAsnTrpIleIleThrAspIle 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---AATCCGCTAGAAACTAGTCTTCCT------
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                                                                                                                                                                                                                                                                                                                               /*tag=  a
/product= "LCAT protein"
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Soezer N,
Heinz E;
                      Keith
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Query Match:
DB:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-651-651-5 (1-546) x ADT99409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Preparing cosmetics
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ArgAspLeuTyrPheHisLysLeuLysLeuThrPheGluThrAlaLeuLysLeuArgGly 186
                                                                         AlaAsnAlaIleValAlaValProTyrAspTrpArgLeuSerProThrLysLeuGluGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ThrGlnLeuArgAlaTrpSerIle-----LeuAspCysProTyrThrProLeuAspPhe 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTTGTTCAGGGGGAGCGGGACATTGCCGAATCGTACGAGCCATTCTCTGTTGGCGAAAAG 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LeulleCysGlyGlyArgThrAlaValGluAspGluThrGluPheHis---GlyAspTyr 38
                                                                                                                                                                                   GlyProLeuSerThrValTrpLysGluTrpLeuLysTrpCysValGluPheGlyIleGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                        -----AGAAAACGACTTTGGGGTAGTTGGACAATGATGAGAGCTCTGGTTATGGACAAG
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                                                 CCAACGAACTCGTTCACGGCTGCTTACGATTGGCGCTTGTCGTATCCCAACCTTGAGGTA
                                                                                                                                                                                                                                                                              LysSerArgProAspSerGlyLeuSerAlaIleThrGluLeuAspProGlyTyrIleThr 126
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              The invention relates to novel isolated nucleic acids encoding diacylglycerol acyltransferases (diacylglycerol O-acyltransferases, DGAT, EC 2.3.1.20) and phospholipid:diacylglycerol acyltransferases (PDAT, EC 2.3.1.158) and the encoded polypeptides. The nucleic acids and methods of the invention may be useful for increasing triacylglycerol (TAG) content in transformed host cells, especially in oleaginous yeasts. The triacylglycerol produced preferably comprises long-chain omega-3/omega-6 polyumanturated fatty acids (PUFAs). The methods allow production of PUFAs with improved nutritional qualities which may be utilized as dietary supplements, particularly for infant formulas, patients undergoing intravenous feeding or for preventing or treating malnutrition, inflammation or high cholesterol. The purified PUFAs may also be incorporated into cooking oils, fate, margarines or other food as a content of the purified purpose that the content of the purified purpose the purpose that the content of the purified purpose the purpose that the purpose the purpose the purpose that the purpose the purpose the purpose the purpose that the purpose the purpose the purpose the purpose that the purpose the purpose the purpose the purpose the purpose the purpose that the purpose the
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acyltransferase (PDAT) protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cannot be synthesized de novo in mammals and must be supplied as part of the diet or derived from linoleic acid or alpha-linolenic acid. There are a variety of commercial sources of PUFAs from natural sources. However, there are disadvantages associated with these methods of production ego heterogeneous oil compositions, pollution, availability fluctuation due to the weather and expense. The current sequence is that of the Yarrowia lipolytica phospholipid:diacylglycerol acyltransferase (PDAT) DNA of the
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CC acyltransferase polypeptide can produce fatty acid esters and/or fatty CC acid thioesters such as triacylglycerols, diacylglycerols, waxesters, CC monoacylglycerols, phospholipids, glycolipids, lysolipids, waxesters, CC acylated carbohydrates and acylated amino acids. Also described: (1) a CC nucleotide sequence molecule (II) comprising at least one promoter region CC which functions in a host, where the promoter region is operably linked to at least one non-CC translated region which functions in a host; (2) a vector comprising (II) (2); (3) a host cell comprising (II) or the vector; (4) producing an CC improved active membrane independent acyltransferase polypeptide, CC comprising providing the above host cell and a growth medium preparing a host cell culture, culturing the host cell culture and harvesting the cacyltransferase polypeptide; (5) a polypeptide obtained by the method in (4), where the polypeptide at least is an improved active membrane independent acyltransferase polypeptide; (6) an oligonucleotide specifically hybridiaing to (I) under stringent conditions; and (7) a kit comprising the above polypeptide are useful in producing structured comprising the above polypeptide are useful in producing structured comprising lipids present in animal and plant raw material. The present condifying lipids present in animal and plant raw material. The present or condifically such active membrane in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleotide sequence encoding an acyltransferase polypeptide comprising least one membrane-spanning region. (I) encodes an improved active membrane independent acyltransferase polypeptide in which at least one amino acid residue of the membrane-spanning region has been deleted and/or substituted as compared to the original acyltransferase polypeptide, where the encoded active membrane independent acyltransferase polypeptide, where the encoded active membrane independent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleotide sequence encoding an improved acyltransferase poluseful for producing structured lipids or fat-soluble molecules, removing undesirable fat or in modifying lipids in animal or pla material.
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                                                                         CATGGAATAGCGGATGATCTTGATGACCCAAAATATAATCATTACAAATATTGGTCGAAT
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                 New nucleotide sequence encoding an improved acyltransferase polypeptide, useful for producing structured lipids or fat-soluble molecules, in removing undesirable fat or in modifying lipids in animal or plant raw material.
                                                                                                                                                                                                                    29-MAY-2002; 2002SE-00001581
29-MAY-2002; 2002US-0383889P
20-JAN-2003; 2003SE-00000142.
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Best Local Similarity:
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|GATTATAATATCGAGGCCAAACATCCTGTTGTAATGGTTCCTGGTGTCATTTCTACGGGA 270
                                                                            IleValAlaValProTyrAspTrpArgLeuSerProThrLysLeuGluGluArgAspLeu 169
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                                                  ATGACGAGTGCTGCGTATGATTGGAGGCTTGCATATTTAGATCTAGAAAGACGCGATAGG 609
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ATGTTCACAAATGGGCCCAGGGTTCACCGTACAACCCTGCCGGAATTAACGTTACT 1503	AGCAAGCAACCTGTATTCCTCACCGAGĠĠĠĠÁCGGAČCĞTTCČĞCTCGTGGCGCATTCA 1443 TrpCysLysAsnTrp	ValProTyrHisSerLeuSer	AspIleIleTyrGluThrGluGlySerLeuValSerArgSerGlyThrValValAspGly 453	GluValGlyTyrTyrPheAlaProSerGlyLysProTyrProAspAsnTrpIleIleThr 433	ProTrpGluArgProProIleLysAsnValPheCysIleTyrGlyAlaHisLeuLysThr 413  GAAGCTCCCCACATGAAAATCTATTGTATATACGGGGTGAACAACCCAACT 1317	LeuLysLysLeuTyrHisAspAspProValPheAsnProLeuThr 393	GlyThrLeuPheLy8AlaIleGluAspTyrAspProAspSerLy8ArgMetLeuHisGln 378	ThrSerMetGluCysGlyLeuProThrLeuLeuSerPheThrAlaArgGluLeuAlaAsp 358	GlulleProSerThrSerValThrGluThrAlaLeuValAsnMet 338	CysAspGluGluGluTyrGlnSerLysTyrSerGlyTrpProThrAsnIleIleAsnIle 323 :::	AsnThrSerTrpThrHisPheSerGlyGlyAlaAlaLysLysAspLysArgValTyrHis 303	TrpLeumetProPheSerLysAsnCysLysGlyAsp 283	GluGlyThrAlaArgLeuLeuSerAsnSerPheAlaSerSerLeu	GlyValThrPheGlyLeuProValSer 256	TyrPheAlaValGlyAlaProLeuLeuGlySerValGluAlaIleLysSerThrLeuSer 247 :::                         :: :: ::       :: ::	LeuGluIleAlaProLysHisTyrLeuLysTrpLeuAspGlnHisIleHisAla 227	IleValPheAlaHigSerMetGlyAgnAsnValPheArgTyrPheLeuGluTrpLeuArg 209 :::	

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phospholipid:diacylglycerol acyltransferase enzymes in the biosynthetic pathway for triacylglycerol production and DNAs encoding them, useful for producing triacylglycerol, or for transforming any cell or organism to increase oil content.
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ProTrpGluArgProProIleLysAsnValPheCysIleTyrGlyAlaHisLeuLysThr 413
                                                    LeuLysLys-----LeuTyrHis-----
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                                                                                        -----AGAGTACATGAGCAGTACTCGTTCGGCTATTCCAAGAATGAAGAAGAG
                                                                                                                  GlyThrLeuPheLysAlaIleGluAspTyrAspProAspSerLysArgMetLeuHisGln
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The present invention describes an enzyme for catalysing (in an acyl-CoA-independent reaction) the transfer of fatty acids from phospholipids to diacylglycerol in the biosynthetic pathway for the production of triacylglycerol (TAG). The enzyme is designated as phospholipid:diacylglycerol acyltransferase (PDAT). The enzyme and the nucleotides encoding them are useful for producing TAG and/or TAG with uncommon fatty acids. The enzyme and the nucleotide are also useful for transforming any cell or organism in order to be expressed in this cell or organism. The present sequence represents the yeast (Saccharomyces cerevisiae) PDAT ORF (open reading frame) nucleotide
                                                                                                                                                                                                                                                                              Phospholipid:diacylglycerol acyltransferase enzymes in the biosynthetic pathway for triacylglycerol production and DNAs encoding them, useful for producing triacylglycerol, or for transforming any cell or organism to increase oil content.
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10-JUN-1999;
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                                                                                                                                                                  TTCATTAATGCAGCAGGGACGCTTCTGGGCGCTCCAAAGGCAGTTCCAGCTCTAATTAGT
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                                    GluGlyThrAlaArgLeuLeuSerAsnSerPheAlaSerSerLeu----
                                                                               GGTGAAATGAAAGATACCATTCAATTAAATACGTTAGCCATGTATGGTTTG-------
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----LeuMetProPheSerLysAsnCysLysGlyAsp 283

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GGGGATATGAAGTCATCTTCAGAGGATGCATTGAAT 1314

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                                                                                                      ProAspSerGlyLeuSerAlaIleThrGluLeuAspProGlyTyrIleThrGlyProLeu
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  TrpCysLysAsnTrp
                                                                                                  AsnAlaGlyProIle-----ThrGlyAspGluThrValProTyrHisSerLeuSer 470
                                                                                                                                                                                                          AspIleIleTyrGluThrGluGlySerLeuValSerArgSerGlyThrValValAspGly
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                                                                                                                                                                                                                                                                                                                                                                   -GAAGCTCCCCACATGAAA---ATCTATTGTATATACGGGGTGAACAACCCAACT
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LeuGlyProLys---ValAsnIleThr
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                      CC nucleotide sequence encoding an acyltransferase polypeptide comprising at CC membrane independent acyltransferase polypeptide in which at least one membrane independent acyltransferase polypeptide in which at least one CC amino acid residue of the membrane-spanning region has been deleted CC and/or substituted as compared to the original acyltransferase colypeptide, where the encoded active membrane independent CC acyltransferase polypeptide can produce fatty acid esters and/or fatty CC acid thioesters such as triacylglycerols, diacylglycerols, waxesters, CC acylated carebohydrates and acylated amino acids. Also described: (1) a nucleotide sequence molecule (II) comprising at least one promoter region cC which functions in a host, where the promoter region is operably linked to at least one (I), which is operably linked to at least one (I), which is operably linked to at least one (I); which is operably linked to at least one (I); which is operably linked to at least one (I); which is operably linked to at least one (I); which is operably linked to at least one non-cC translated region which functions in a host; (2) a vector comprising (II); (3) a host cell comprising (II) or the vector; (4) producing an CC improved active embrane independent acyltransferase polypeptide, (5) a polypeptide obtained by the method in colorate the polypeptide; (5) a polypeptide obtained by the method in condens acyltransferase polypeptide at least is an improved active membrane independent independent acyltransferase polypeptide at least is an improved active membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleotide sequence encoding an improved acyltransferase polypeptide, useful for producing structured lipids or fat-soluble molecules, in removing undesirable fat or in modifying lipids in animal or plant raw material.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a nucleotide sequence (I) derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5; SEQ
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                                                                                                                                                                                          environmental
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stress;

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483

1728

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CC compared to a corresponding plant cell with altered metabolic activity is altered by transformed wild type plant cell (where the metabolic activity is altered by transformed wild a SRP coding CC uncleic acid and results in increased tolerance and/or resistance to an environmental stress as compared to a corresponding non-transformed wild type plant cell above (and which is a monocot or dicot plant generated from the plant cell above (and which is a monocot or dicot plant, or a gymnosperm plant), a seed produced by a transgenic plant above (where the seed is genetically CC resulting in an increased tolerance to environmental stress as compared to a corresponding non-transformed wild type plant), a nucleic acid molecule above (comprising one or more regulatory elements, where expression of the SRP CC construct which confers the expression of the nucleic acid molecule above (comprising one or more regulatory elements, where expression of the SRP CC corresponding non-transformed wild type host cell), a vector comprising the nucleic acid molecule above or the nucleic acid construct, a host cell which has been transformed wild type host cell), a vector comprising the nucleic acid molecules above, or the nucleic acid construct, an a solated Stress Related protein (SRP) selected from the amino acid sequences fully given in the specification and/or its homologues, a method of producing a transgenic plant with altered metabolic activity compared to a corresponding non-transformed wild type plants for increased tolerance to environmental stress in plants compared to a corresponding non-transformed wild type plant cell; compared to a corresponding non-transformed wild type plant for increased tolerance of a plant tolerance to environmental stress in plants towards increased tolerance and/or resistance to environmental compared to a plant transformed with the nucleic acids one abiotic stress; in plant altered metabolic activity and/or a SRP encoding nucleic acids or its bomologues are useful as markers for selection of p
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                                                         US-09-651-651-5
                                                                                                                                                                                            Percent Similarity:
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                                                                                                                                                                Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-2003;
30-SEP-2003;
                                                                                                                                                                                                                                                                                                                                                                              homologues are useful as markers for selection of plants or plant cells with increased tolerance to environmental stress, or for detection of stress in plants or plant cells. The nucleic acids are useful for producing transformed plants with altered metabolic activity resulting increased tolerance and/or resistance to an environmental stress (drought, heat, cold and salt) as compared to a corresponding nontransformed wild-type plant cell. The present sequence is a yeast gene encoding an SRP of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-766883/75.
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496 GATTATAATATCGAGGCCAAACATCCTGTTGTAATGGTTCCTGGTGTCATTTCTACGGGA 555
           359 GlyThrLeuPheLysAlaIleGluAspTyrAspProAspSerLysArgMetLeuHisGln 378
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                                                                                                                                                                                            AACAACACTGACACATAC----
                                                                                                                                                                                                                                                                                                                                                             CysAspGluGluGyrGlnSerLysTyrSerGlyTrpProThrAsnIleIleAsnIle 323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GluGlyThrAlaArgLeuLeuSerAsnSerPheAlaSerSerLeu-------
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                                                                                                                                      ThrSerMetGluCysGlyLeuProThrLeuLeuSerPheThrAlaArgGluLeuAlaAsp 358
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                                                                                           TTATCGATATCACCTGAATGGCTCCAAAGA 144
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Search completed: November 22, 2005, 11:10:37 Job time: 679 secs	Qy 484MetAlaProGlnProGlu 489	Qy 471 TrpCysLysAsnTrpLeuGlyProLysValAsnIleThr	Qy 454 AsnalaGlyProlleThrGlyAspGluThrValProTyrHisSerLeuSer	Qy 434 AspileIleTyrGluThrGluGlySerLeuValSerArgSerGlyThrValValAspGly 453	Qy 414 GluValGlyTyrTyrPheAlaProSerGlyLy8ProTyrProAspAsnTrpIleIleThr 433	Qy 394 ProTrpGluArgProProIleLysAsnValPheCysIleTyrGlyAlaHisLeuLysThr	Qy 379 LeuLysLysLeuTyrHisAspAspProValPheAsnProLeuThr 393	
		LeuGlyProLysValAsnIleThr 483	GluThrValProTyrHisSerLeuSer 470 	SerArgSerGlyThrValValAspGly 453 :::    ::: GCTCTGAATTTGACCATCGACTACGAA 1668	ProTyrProAspAsnTrpIleIleThr 433	CysIleTyrGlyAlaHisLeuLysThr 413            	ABDABDPTOVAIPheABDPTOLeuThr 393 	

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-Q=/Ggn2 1/USP70_spool/US09651651/runat 18112005_101831_20277/app_query.fasta_1.711
-DB=Issued Pateents NA -QFWT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=Dits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DCCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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-DEV TIMEDUT=120 -MANL TIMEOUT=30 -THREADS=1 -NORM=pct -LORGELOG
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1: /cgn2_6/ptodata/l/ina/1_COMB.seq:*

2: /cgn2_6/ptodata/l/ina/5_COMB.seq:*

3: /cgn2_6/ptodata/l/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/l/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/l/ina/PTUS_COMB.seq:*

6: /cgn2_6/ptodata/l/ina/PTUS_COMB.seq:*

7: /cgn2_6/ptodata/l/ina/PCOMB.seq:*

8: /cgn2_6/ptodata/l/ina/PCOMB.seq:*

9: /cgn2_6/ptodata/l/ina/RE_COMB.seq:*
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Sequence 19, Appl
Sequence 3703, Ap
Sequence 30, Appl
Sequence 30, Appl
Sequence 12, Appl
Sequence 15, Appl
Sequence 17, Appl
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Sequence 16, Appli Sequence 18, Appli Sequence 19, Appli Sequence 9, Appli Sequence 9, Appli Sequence 7, Appli Sequence 29, Appli Sequence 30, Appli Sequence 15, Appli Sequence 1602, Appli Sequence 1802, Appli Sequence 1802, Appli Sequence 1802, Appli Sequence 1802, Appli Sequence 1802, Appli Sequence 2010, Appli Sequence 210, Appli Sequence 1802, Appli Sequence 1802, Appli Sequence 1802, Appli Sequence 1802, Appli Sequence 1802, Appli Sequence 31, Appli Sequence 18, Appli Sequence 18, Appli Sequence 2010, Appli Sequence 2010, Appli Sequence 3, Appli Sequence 1, Appli Sequence 1, Appli	`@`@

## ALIGNMENTS

RESULT 1 US-09-248-796A-1147

Patent No. 6747137

Sequence 1147, Application US/09248796A

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GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND THERAPBUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPBUTICS
FILE REFERENCE: 107196.132
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR APPLICATION NUMBER: US 60/096,4
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                                                                                                                                                                                                                                                                                                                                              GTCGATATGTTGAGATCATTTGGTGGTATTGCCAGTATGATACCT-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AsnAsnValPheArgTyrPheLeuGluTrpLeuArgLeuGluIleAlaProLysHisTyr 217
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TCACAAATTATTATTATTTTTGAAATGG-----GTTGAAGCCAAAGGAGAATATTAT 1131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTTGAAATTGTCAAACAATTGACAGGTAAAAAATCAGTATTAGTGGGCCATTCAATGGGT 1077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAAAACTTAGCTGTGATTGGTTATGGACCCAATAATATGATTAGTGCCTCGTATGACTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LysTrpCysValGluPheGlyIleGluAlaAsnAlaIleValAlaValProTyrAspTrp 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GATTTTTTCATGGCGGGTAT------TGGATTTGGAATAAAATTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ThrGluLeuAspProGlyTyrIleThrGlyProLeuSerThrValTrpLysGluTrpLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TyrAsnGlnThrAspHisProGluCysLysSerArgProAspSerGlyLeuSerAlaIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GATAAAACT-----TGTTGGCTTAGACATATCATGTTAGATACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTGGTCATTTCCGGAAAAGATTATGGGGGATCATTTTATATGTTAAGAACTATGGTTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ThrProLeu-------AspPheAsnProLeuAspLeuValTrpLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlyPheAlaSerThrGlnLeuArgAlaTrpSerIleLeu------AspCysProTyr 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTTGAAAATCTGAAAAATTTCACAGCTGACCATAATGTA-----GTTATGGTCCCT
                                                                                                                                                                                                                                                                                                                                                                                       ArgLeuLeuSerAsnSerPheAlaSerSerLeuTrpLeuMetProPheSerLysAsnCys 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGTAACGGAGGACCTAATTGGGTCGAAGATTACGTTGAAGCATTTGTTAATATTAGTGGA 1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PheGluThrAlaLeuLysLeuArgGlyGlyProSerIleValPheAlaHisSerMetGly 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AspThrThrLysLeuLeuSerAlaValAsnCysTrpPheLysCysMetValLeuAspPro
                                                                                                                                                           GTTGCATTTGATACCGAAAAAGGAAGATATTGGTGAAAAAGAAAAAGATCATTT------
                                                                                                                                                                                                      Val---TyrHisCysAspGluGluGluTyrGlnSerLysTyrSerGlyTrpProThrAsn
                                                                                                                                                                                                                                                      AAAGGTGGTGACAAAATATGGGGGAATTTGACT-----TATGCTCCTGATGATGAAATA 1410
                                                                                                                                                                                                                                                                                              LysGlyAspAsnThrSerTrpThrHisPheSerGlyGlyAlaAlaLysLysAspLysArg 300
                                                                                                                                                                                                                                                                                                                                                                                                                                         GTACAATTAAATGCCTTAGCGGTGTATGGATTAGAGCAATTTTTCAGTAGACGTGAAAGA
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                                                                                                             IleIleAsnIleGluIleProSerThrSerValThrGluThrAlaLeuValAsnMetThr 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----ValSerGluGlyThrAla
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                                                                     -GGATCATTTATTCAATACAAAACTGCCAATGACTCT 1497
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Query Match:
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US-09-402-532-14
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  US-09-651-651-5 (1-546) x US-09-402-532-14 (1-1137)
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                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: TANIYAMA, YOShio
TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION
FILE REFERENCE: 2456USOP
                                                                                                                                                                                                                                                                                              SEQ ID NO 14
LENGTH: 1137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 14, Application US/09402532 Patent No. 6498019
                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/402,532
CURRENT FILING DATE: 1999-10-04
EARLIER APPLICATION NUMBER: PCT/JP98/01643
EARLIER FILING DATE: 1998-04-09
EARLIER APPLICATION NUMBER: JP 10-010289
EARLIER FILING DATE: 1998-01-22
EARLIER FILING DATE: 1998-01-22
EARLIER FILING DATE: 1997-07-10
                                                                                                                                                                                                                                                                                                                                                                                           EARLIER APPLICATION NUMBER: JP 9-093355 EARLIER FILING DATE: 1997-04-11
                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
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ORGANISM: Murine
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22 GTGCTGGTGCCTGGTGATTTGGGTAACCAGTTGGAAGCA-----AAGCTGGATAAGCCA
                                                                                                                                                                                                                                                                                                            lTyrHisCysAspGluGluGluTyrGlnSerLysTyrSerGlyTrpProThrAsnIleIl 321
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                                                                                                                                tGluCysGlyLeuProThrLeuLeuSerPheThrAlaArgGluLeuAlaAspGlyThrLe 361
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  -CACCGGTTCTTCCG 800
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Qy 6	Qy 44 Db 121	US-09-651-65	Alignment Sc Pred. No.: Score: Secrent Simi Best Local S Query Match: DB:	RESULT 3 US-09-402-532-1 Sequence 19, Sequence 19, Sequence 19, GENERAL INFO APPLICANT: 7 ITTLE OF IN FILE REFERE CURRENT FILL CURRENT FILL CURRENT FILL EARLIER APPL EARLIER FILL EARLIER FILL EARLIER FILL EARLIER FILL EARLIER FILL EARLIER FILL SARLIER FILL EARLIER FILL EARLIER FILL EARLIER FILL EARLIER FILL SARLIER FILL EARLIER FILL EARLIER FILL EARLIER FILL EARLIER FILL SARLIER FILL EARLIER FILL GARLIER FILL OMMER OF SI SOFTWARE: SOFTWARE: SOFTWARE: SOFTWARE: GOGANISM: N	10	0у 512		Qy 475 Дb 1023	Qy 455 Db 976	Qy 435 Db 949	Qy 415 Db 921	86	Qy 380 Db 801 Ov 395	
4	IleIleIle :::::::: GTGCTGGTG	1-5 (1-546) x US-09-402-53	No.: 1.83e-17 No.: 234.00 :: 234.00 :nt Similarity: 35.81% Local Similarity: 22.70% - Match: 7.89%	Application US/0940253 (A98019 GA98019 GA98019 ENCE: 245GUSOP ENCE: 245GUSOP PLICATION UNMBER: US/09/ LING DATE: 1999-10-04 PLICATION NUMBER: PCT/JP FLICATION NUMBER: JP 10- LING DATE: 1998-01-22 PLICATION NUMBER: JP 9-0 PLICATION NUMBER: JP 9-0 LING DATE: 1997-07-10 PLICATION NUMBER: JP 9-0 PLI		nMetThrLysAlaProArgV	~	pLeuGly       GCAGAGCCGCCAAGAG	aGlyProIleThr		lGlyTyrTyrPheAlaProSerGl :::   ::: CTCTTTCTACTAC			
TyrThrProLeuAspPheAs	lnLeuArgAlaTrpS       AGTTGGAAGCA	532-19 (1-1236)	Length: 1236 Matches: 116 Conservative: 67 Mismatches: 154 Indels: 175 Gaps: 26	32 , ITS PRODUCTION AND USE /402,532 P98/01643 -010289 184885	ACGTGTG 1125	522	nValAspHisGluHisGlySerA ;	ProLysValAsnIleThrMetAlaProGlnProGluHisAspG 	GlyAspGluThrValProTyrHisSerLeuSerTrpCysLysAsnTr        	IleTyrGluThrGluGlySerLeuValSerArgSerGlyThrValValAspGlyAsnAl         :::         :::	yLysProTyrProAspAsnTrpI ::: ::       -GAGAGCTTTCCTGAT	:     :::        gcactgcttgtatggcactggtg	PheAsnPr     GTTCATGCGGCAGGACACAGAAG	
AsnProLeuAspLeu 74	erIleLeuAspCysPro 63        AAGCTGGATAAGCCA 174						SerAspIleIleAlaAs 512 :::::::      arrgacarggraagggaa 1094	roGluHisAspGl 492        GCGAGCAC 1077	rpCysLysAsnTr 475 .    :::    AGTGCCAAGCCTG 1022	alAspGlyAsnAl 455    ::: GCTTCGGCGAT 975	leIleThrAspIl 435		AsnProLeuThrProTr 395     GAAGGGCTGGTTGAAGC 860 HisLeuLysThrGluVa 415	ر د

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233 CTCTGGCTGAATCTGGAACTGCTTCTGCCTGTTATCATTGACTGCTGGATTGACAATATC
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395 pGluArgProProIleLysAsnValPheCysIleTyrGlyAlaHisLeuLysThrGluVa 415
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                                                                        GGACATCGGTTTCGAAGATGGCTGGTTCATGCGGCAGGACACAGAAGGGCTGGTTGAAGC
                                                                                                          sLysLeuTyrHisAspAspProValPhe------AsnProLeuThrProTr
                                                                                                                                                                                                                                                                                                        tGluCysGlyLeuProThrLeuLeuSerPheThrAlaArgGluLeuAlaAspGlyThrLe 361
                                                                                                                                                                                                                                                                                                                                                   ----GTATACACACCCACGACTAACTACACG-------
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                                                                                                                                                                 -----CTCCGGGACTAT------CACCGGTTCTTCCG
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75 ValTrpLeuAspThrThrLysLeuLeuSerAlaValAsnCysTrpPheLysCysMet 93 :::          261 ATCTGGCTGGATCTCAACATGTTCCTACCCCTTGGGGTAGACTGCTGG 308	57TrpSerIleLeuAspCysProTyrThrProLeuAspPheAsnProLeuAspLeu 74	44 IleIleIleProGlyPheAlaSerThrGlnLeuArgAla	09-651-651-5 (1-546) x US-09-949-016-3703 (1-1354)	Alignment Scores: 1.94e-16 Length: 1354  Pred. No.: 226.00 Matches: 114  Percent Similarity: 35.82% Conservative: 54  Best Local Similarity: 24.31% Mismatches: 153  Query Match: 7.62% Indels: 148  Ouery Match: 3 Gaps: 25	REFERENCE: CLO01307 TO APPLICATION NUMBER: US/09/949,016 TILING DATE: 2000-04-14 APPLICATION NUMBER: 60/241,755 FILING DATE: 2000-10-20 APPLICATION NUMBER: 60/237,768 FILING DATE: 2000-10-03 APPLICATION NUMBER: 60/231,498 FILING DATE: 2000-09-08 APPLICATION NUMBER: 60/231,498 FILING DATE: 2000-09-08 APPLICATION NUMBER: 60/231,498 TILING DATE: 2000-09-08 APPLICATION NUMBER: 60/231,498 APPLICATION N	RESULT 4  US-09-949-016-3703  , Sequence 3703, Application US/09949016  ; Patent No. 6812339  ; GENERAL INFORMATION:  ; APPLICANT: VENTER, J. Craig et al.  ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  ; TITLE OF INVENTION: WITH HIMAN DISEASE. METHODS OF DETECTION AND USES THEREOF	512 nMetThrLyBAlaProArgValLyBTyrIle 522	492 ySerAspValHisValGluLeuAsnValAspHisGluHisGlySerAspIleIleAlaAs 512 ::::::      1177ATTGAGATGCTAGCCAA 1193	475 pLeuGlyProLysValAsmIleThrMetAlaProGlnProGlnHisAspG1 492		435 elleTyrGluThrGluGlySerLeuValSerArgSerGlyInrvalValAspolyAsHA1 433	CTCTTTCTACTACGAGAGCTTTCCTGAT	laProSerGlyLysProTyrProAspAsnTrpIleIleThrAspIl	960 CATGACGCCACCCGGGGTGGAGCTGCACTGCTTGTATGGCACTGGTGTTCCCCACGCCAAA 1019

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlyAspAsnThrSerTrpThrHisPheSerGlyGlyAlaAlaLysLysAspLysArgVal 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ArgTyrPheLeuGluTrpLeuArgLeuGluIleAlaProLysHisTyrLeuLysTrpLeu 221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AsnIleGluIleProSerThrSerValThrGluThrAlaLeuValAsnMetThrSerMet 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GACCGCTTTATTGATGGCTTCATCTCTTGGGGCTCCCTGGGGTGGCTCCATCAAGCCC 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AspGlnHisIleHisAlaTyrPheAlaValGlyAlaProLeuLeuGlySerValGluAla 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTCTATTTCCTG-----CTGCGCCAGCCCCAGGCC-----TGGAAG 680
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                                                                                          SerGlyLysProTyrProAspAsnTrpIleIleThrAspIleIleTyrGluThrGluGly 441
                                                                                                                                                                                                   AsnValPheCysIleTyrGlyAlaHisLeuLysThrGluValGlyTyrTyrPheAlaPro 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GluCysGlyLeuProThrLeuLeuSerPheThrAlaArgGluLeuAlaAspGlyThrLeu 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCACCACCTCCCCTGGATGTTTCCCTCTCGCATGGCG---TGGCCTGAGGACCACGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TyrHisCysAspGluGluGluTyrGlnSerLysTyrSerGlyTrpProThrAsnIleIle 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LeuLeuSerAsnSerPheAlaSerSerLeuTrpLeuMetProPheSerLysAsnCysLys 281
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SerLeuValSerArgSerGlyThrValValAspGlyAsnAlaGlyProIleThrGlyAsp 461
                                                       CACGGCTTCCCCTACACGGACCCT-----GTGGGTGTGCTCTATGAG-----
                                                                                                                                                                                                                                                                                                                                                                                             TTCTTTGCAGACCTGCACTTTGAG----GAAGGCTGGTACATGTGGCTGCAGTCACGTGAC 980
                                                                                                                                                                                                                                                                                                                                                                                                                                               PheLysAlaIleGluAspTyrAspProAspSerLysArgMetLeuHisGlnLeuLysLys 381
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                                                                                                                                                                                                                                                                                 LeuTyrHisAspAspProValPheAsnProLeuThrProTrpGluArgProProIleLys 401
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Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                  Alignment Scores:
                                                      score:
                                                                                                                    US-09-054-272-33
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Patent No. 6692909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                        NAME: Granahan, Patricia REGISTRATION NUMBER: 32,227 REFERENCE/DOCKET NUMBER: WH TELECOMMUNICATION INFORMATION: TELEPHONE: 781-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Window
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Daley, George Q.
APPLICANT: Cargill, Michele
APPLICANT: Ireland, James S.
APPLICANT: Rozen, Steven G.
TITLE OF INVENTION: CODING SEQUENCE POLYMORPHISMS
TITLE OF INVENTION: IN VASCULAR PATHOLOGY GENES
NUMBER OF SEQUENCES: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 01-APR-CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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ADDRESSEE: HAMILTON, BROOK,
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                                                                                                                                                                                 FEATURE:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
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                                                                                                                                  OTHER INFORMATION:
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Daley, George Q.
Cargill, Michele
Ireland, James S.
Rozen, Steven G.
INVENTION: CODING SE
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Percent Similarity:
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US-09-402-532-12
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CURRENT FILING DATE: 1999-10-04
EARLIER APPLICATION NUMBER: PCT/JP98/01643
EARLIER FILING DATE: 1998-04-09
EARLIER APPLICATION NUMBER: JP 10-010289
EARLIER FILING DATE: 1998-01-22
EARLIER APPLICATION NUMBER: JP 9-184885
EARLIER APPLICATION NUMBER: JP 9-184885
EARLIER APPLICATION NUMBER: JP 9-093355
EARLIER APPLICATION NUMBER: JP 9-093355
EARLIER APPLICATION NUMBER: JP 9-093355
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LENGTH: 1137
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TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION
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                                                                      uGluArgAspLeuTyrPheHisLysLeuLysLeuThrPheGluThrAlaLeuLysLeuAr 185
                                                                                                          ACGGGGTGAGGATGTCCCAAGGGGCTCCCTATGACTGGCGCCGAGCCCCA------AA 404
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Patent No. 6498019

GENERAL INFORMATION:

APPLICANT: TENIYAMA, YOSHIO

TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND FILE REFERENCE: 2456USOP

CURRENT APPLICATION NUMBER: US/09/402,532

CURRENT FILING DATE: 1999-10-04

EARLIER APPLICATION NUMBER: PCT/JP98/01643

EARLIER FILING DATE: 1998-04-09

EARLIER APPLICATION NUMBER: JP 10-010289

EARLIER APPLICATION NUMBER: JP 9-184885

EARLIER FILING DATE: 1998-01-22

EARLIER APPLICATION NUMBER: JP 9-093355

EARLIER FILING DATE: 1997-07-10

EARLIER APPLICATION NUMBER: JP 9-093355

EARLIER FILING DATE: 1997-04-11

NUMBER OF SEQ ID NOS: 43
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LENGTH: 1146
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ORGANISM: Human
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                                    uGluTrpLeuArgLeuGluIleAlaProLysHisTyrLeuLysTrpLeuAspGlnHisIl
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                                                                                                                                                                                                                                                                             eGluAlaAsnAlaIleValAlaValProTyrAspTrpArgLeuSerProThrLysLeuGl 165
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                                                                                    TGGGGGCCCCGTGGTGCTGGTCCCCACAGTATGGGCAACATGTACACGCTCTACTTTCT
                                                                                                          gGlyGlyProSerIleValPheAlaHisSerMetGlyAsnAsnValPheArgTyrPheLe
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RESULT 9
US-09-402-532-17
US-09-402-532-17
; Sequence 17, Application US/09402532
; Patent No. 6498019
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; GENERAL INFORMATION:
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APPLICANT: Taniyama, Yoshio TITLE OF INVENTION: NOVEL PROTEIN, FILE REFERENCE: 2456USOP
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CURRENT FILING DATE: 1999-10-04
EARLIER APPLICATION NUMBER: PCT/JP98/01643
EARLIER FILING DATE: 1998-04-09
EARLIER APPLICATION NUMBER: JP 10-010289
EARLIER FILING DATE: 1998-01-22
EARLIER APPLICATION NUMBER: JP 9-184885
EARLIER FILING DATE: 1997-07-10
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: JP 9-093355
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TYPE: DNA
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                                                                                                                                                                                                 uGluTrpLeuArgLeuGluIleAlaProLysHisTyrLeuLysTrpLeuAspGlnHisIl
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     rLeuSerGlyValThrPheGlyLeuProVal---SerGluGlyThrAlaArgLeuLeuSe 264
                                                                                                   eHisAlaTyrPheAlaValGlyAlaProLeuGlySerValGluAlaIleLysSerTh
                                                      CCGGGCCTTCGTGTCACTGGGTGCGCCCCTGGGGGGGGGCGTGGCCAAGACCCCTGCGGGGTCCT
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o. 6916648
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Filvaroff, Ellen
Fong, Sherman
                                                                                  Desnoyers, Luc
                                                                                                    Baker Kevin P.
Botstein, David
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PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR FILING DATE: 1997-11-21
PRIOR FILING DATE: 1998-03-10
PRIOR FILING DATE: 1998-03-11
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR PILING DATE: 1998-03-11
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PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C65
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DR FILING DATE: 1998-03-20
DR APPLICATION NUMBER: 60/078936
OR FILING DATE: 1998-03-20
DR APPLICATION NUMBER: 60/078939
DR APPLICATION NUMBER: 60/078939
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APPLICATION NUMBER: 60/077649
FILING DATE: 1998-03-11
APPLICATION NUMBER: 60/077791
                                                FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079920
FILING DATE: 1998-03-30
APPLICATION NUMBER: 60/079923
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FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079663
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FILING DATE: 1998-03-26
APPLICATION NUMBER: 60/079664
FILING DATE: 1998-03-27
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APPLICATION NUMBER: 60/078004
FILING DATE: 1998-03-13
             FILING DATE: 1998-03-30
APPLICATION NUMBER: 60/080105
                                                                                                      APPLICATION NUMBER: 60/079786
FILING DATE: 1998-03-27
                                                                                                                                          APPLICATION NUMBER: 60/079728 FILING DATE: 1998-03-27
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FILING DATE:
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Hillan, Kenneth J
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Grimaldi,
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Goddard, Audrey
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FILING DATE: 1998-04-08 APPLICATION NUMBER: 60/081071

APPLICATION NUMBER: 60/081049

1998-04-08 1998-04-01 1998-04-00 1998-04-01

60/081070

APPLICATION NUMBER: FILING DATE: 1998-0

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PRIOR PRIOR PRIOR

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NUMBER:

60/081195

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APPLICATION : FILING DATE: APPLICATION FILING DATE: APPLICATION FILING DATE:

NUMBER: 60/081952 NUMBER: 60/081819

APPLICATION NUMBER: 60/081838

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1998-04-1998-04-15 1998-04-15 1998-04-15 1998-04-09 1998-04-09

APPLICATION NUMBER:

60/082568

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APPLICATION NUMBER: 60/082569

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PRIOR PRIOR PRIOR PRIOR PRIOR

APPLICATION N FILING DATE: APPLICATION N FILING DATE:

NUMBER: 60/081955

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60/081229

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NUMBER: 60/080333 NUMBER: 60/080328

APPLICATION NUMBER: 60/080334

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60/080327

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NUMBER: 60/080194

1998-03-3 1998-03-31

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60/080165 60/080107

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DR FILING DATE: 1998-05-07
DR APPLICATION NUMBER: 60/085339
DR FILING DATE: 1998-05-13
DR APPLICATION NUMBER: 60/085338
DR FILING DATE: 1998-05-13
DR FILING DATE: 1998-05-13
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DR APPLICATION NUMBER: 60/085689
DR FILING DATE: 1998-05-15
DR APPLICATION NUMBER: 60/085579
DR FILING DATE: 1998-05-15
DR APPLICATION NUMBER: 60/085580
DR FILING DATE: 1998-05-15
DR APPLICATION NUMBER: 60/085573
DR FILING DATE: 1998-05-15
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DR APPLICATION NUMBER: 60/085704
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DR APPLICATION NUMBER: 60/085697
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FILING DATE: 1998-05-13
APPLICATION NUMBER: 60/085582
FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085700
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APPLICATION NUMBER: 60/084640
FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/084598
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APPLICATION NUMBER: 60/084366
FILING DATE: 1998-05-05
APPLICATION NUMBER: 60/084414
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APPLICATION NUMBER: 60/084639
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                                                                                                                                                                                                          TyrThrProLeuAspPhe
                                                                                                                                                                                                                                        GTGCTGGTCCCTGGTGATTTGGGTAACCAACTGGAAGCC
GTCCCTGGCTTTGGGAAGACCTTCTCACTGGAGTTCCTGGACCCCAGCAAAAGCAGCGTG
                                                                                                                                       AspThrThrLysLeuLeuSerAla---ValAsnCysTrpPheLysCysMetValLeuAsp
                                                                              ProTyrAsnGlnThrAspHisProGluCysLysSerArgProAspSer--------
                                                                                                                                                                             ---ACAGTGGTGCACTACCTCTGCTCCAAGAAGACCGAAAGCTACTTCACAATCTGGCTG
                               -GlyLeuSer---
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Matches:
Conservative:
Mismatches:
Indels:
                             AlaIleThrGluLeuAspProGlyTyrIleThr---
                                                           AGGGCCACCCAGTTTCCTGATGGTGTGGATGTACGT
                                                                                                                                                                                                                                                                                                                              Gaps:
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R FILING DATE: 1998-04-29 APPLICATION N FILING DATE: APPLICATION N FILING DATE: APPLICATION FILING DATE:
APPLICATION PILING DATE: APPLICATION I FILING DATE: APPLICATION FILING DATE: APPLICATION NUMBER: 60/082700 FILING DATE: 1998-04-22 APPLICATION NUMBER: FILING DATE: 1998-04 APPLICATION NUMBER: 60/082704 FILING DATE: FILING DATE: APPLICATION APPLICATION APPLICATION FILING DATE: APPLICATION FILING APPLICATION APPLICATION FILING DATE: FILING DATE: DATE: 1998-04-29 NUMBER: NUMBER: 60/083500: 1998-04-29 NUMBER: 60/083559 NUMBER: 60/083554 NUMBER: 60/083545 NUMBER: 60/083499 NUMBER: NUMBER: NUMBER: 60/083392 NUMBER: NUMBER: NUMBER: 60/082796 NUMBER: 60/082797 1998-04-29 1998-04-22 1998-04-22 1998-04-1998-04-29 1998-04-23 1998-04-29 1998-04-1998-04-29 1998-04-27 60/083742 60/083558 60/083496 60/083495 60/083322 60/083336 60/082804

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                                                                                                                                                                                                                                                                                                                                                                                                                                          384 sAsp-----AspProValPheAsnProLeuTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             364 alleGluAspTyrAspProAspSerLysArgMetLeuHisGlnLeuLysLysLeuTyrHi 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   344 yLeuProThrLeuLeuSerPheThrAlaArgGluLeuAlaAspGlyThrLeuPheLysAl 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        264 rAsnSerPheAlaSerSerLeuTrpLeuMetProPheSerLysAsnCysLysGlyAspAs
473 BABnTrpLeuGlyProLysValAsnIleThrMetAlaProGlnProGluHisAspGlySe 493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          uIleProSerThrSerValThrGluThrAlaLeuValAsnMetThrSerMetGluCysGl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gGlyGlyProSerIleValPheAlaHisSerMetGlyAsnAsnValPheArgTyrPheLe
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                                                                                                                                                                                                                                               GGAAGCCACGATGCCACCTGGCGTGCAGCTGCACTGCCTCTATGGT------
                                                                                                                                                                                                                                                                                                                                                                                                 GGACATCGGCTTTGAAGATGGCTGGCTCATGCGGCAGGACACA-----GAAGGGCTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----CCTGAGAAGGTGTTCGTGCAGACACCCACAATCAACTACACA--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sAspGluGluGluTyrGlnSerLysTyrSerGlyTrpProThrAsnIleIleAsnIleGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTACACATGGTCA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nThrSerTrpThrHisPheSerGlyGlyAlaAlaLysLysAspLysArgValTyrHisCy
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                                                                                      YABNAlaGlyProIleThrGlyABpGluThrValProTyrHi8SerLeuSerTrpCy8Ly
                                                                                                                                  ----TACTATGAG-----AGCTTCCCTGACCGTGACCCTAAAATCTGCTTTGG
                                                                                                                                                                        rAspIleIleTyrGluThrGluGlySerLeuValSerArgSerGlyThrValValAspGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -CTGCGGGACTAC----
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                                             GGCGATGGTACTGTGAACTTGAAGAGTGCCCTGCAGTGCCA
                                                                                                                                                                                                                        -ACTGGCGTCCCCACACCAGACTCCTTC-----
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APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C74

CURRENT APPLICATION NUMBER: US/10/020,445A

CURRENT FILING DATE: 2001-10-24

PRIOR APPLICATION NUMBER: 09/91858

PRIOR APPLICATION NUMBER: 09/91858

PRIOR APPLICATION NUMBER: 60/062250

PRIOR APPLICATION NUMBER: 60/062250

PRIOR APPLICATION NUMBER: 60/06249

PRIOR APPLICATION NUMBER: 60/064249

PRIOR APPLICATION NUMBER: 60/064311

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PRIOR APPLICATION NUMBER: 60/066364

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PRIOR APPLICATION NUMBER: 60/074650
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Patent No. 6962797
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
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              APPLICATION NUMBER: 60/078886 FILING DATE: 1998-03-20
                                                                                            APPLICATION NUMBER: 60/077791
FILING DATE: 1998-03-12
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                                                                           APPLICATION NUMBER: 60/078004
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Wood, William
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Shelton, David L.
Stewart, Timothy A.
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Hillan, Kenneth J
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Grimaldi, J. Christopher
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Gerritsen, Mary E.
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Botstein, David
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APPLICATION NUMBER: 60/078910
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R FILING DATE: 1998-03-30

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1998-03-27

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NUMBER: 60/079689

APPLICATION NUMBER: 60/079656
FILING DATE: 1998-03-26
APPLICATION NUMBER: 60/079664
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NUMBER: 60/079294

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NUMBER: 60/080165

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NUMBER: 60/080107

APPLICATION NUMBER: 60/080194
FILING DATE: 1998-03-31
APPLICATION NUMBER: 60/080327
FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/080328

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60/080105 60/079923 60/079920

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APPLICATION NUMBER: 60/083336
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Alignment Scores:
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FILING DATE: 1998-0-APPLICATION NUMBER: FILING DATE: 1998-0-

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947-57 Scores: 5.12e-14 210.00	ORGANI FEATUR NAME/K LOCATI OTHER	SOFTWARE: Patent SEQ ID NO 57 LENGTH: 2687 TYPE: DNA	APPLICATION NUMBER 199 FILING DATE: 199 OF SEQ ID NOS: 37		; EARLIER APPLICATION NUMBER: 60/094,657 ; EARLIER FILING DATE: 1908-07-30 ; EARLIER APPLICATION NUMBER: 60/095,486 ; EARLIER APPLICATION NUMBER: 08-08-08-08-08-08-08-08-08-08-08-08-08-0		APPLICAN TITLE OF FILE REF	US-09-489-847-57 US-09-489-847-57 ; Sequence 57, Application US/09489847 ; Patent No. 6476195 ; CENERAL INFORMATION:	Db 1217 CACCACCCTGGCCTATCTGAAACGTGTG 1244	493 rABBYWALHSWALGLULGUABHYWALABPH   ::	473 \$A\$nTrpLeuGlyProLy8ValA\$nIleThrMetAlaProGlnProGluHi8A\$pGlySe	Oy 453 yAsnAlaGlyProIleThrGlyAspGluThrValProTyrHisSerLeuSerTrpCysLy 473  :::	Qy 433 rAspIleIleTyrGluThrGluGlySerLeuValSerArgSerGlyThrValValAspGl 453	Qy 413 rGluValGlyTyrTyrPheAlaProSerGlyLysProTyrProAspAsnTrp11e11e1n 433	393 rProTrpGluArgProProIleLysAsnValPheCysIleTyrclyAlsHisLeuLysTh        974 GGAAGCCACGATGCCACCTGGCGTGCACTGCCTCTATGGT		Qy 364 alleGluAspTyrAspProAspSerLysArgMetLeuHisGlnLeuLysLysLeuTyrHi 384 :::        Db 894 -CTGCGGGACTAC

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	6	Alignment Scores: 1.78e-14 Length: 1233  Pred. No.: 209.00 Matches: 115  Percent Similarity: 33.79\$ Conservative: 58  Best Local Similarity: 22.46\$ Mismatches: 154  Query Match: 3.05\$ Indels: 186  DB: Gaps: 25	386ABPPTOVAIPHAABNPTOLEUTHTPTOTTGUANTGPTOFTOILELY  938 GCGGCAGCACACA	Qy 374 gMetLeuHisGlnLeuLysLysLeuTyrHisAsp	Db 882CTGCGGGACTAC
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870	ABILIEGIUIIEFFOSERINTSERVALINIGIUIIFALAURUVALABINWETINISERWEC	829
828		828
21	TyrHisCysAspGluGluGluTyrGlnSerLysTyrSerGlyTrpProThrAsnIleIle 321	302
828	AACTACACATGGTCA	814
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813	GAGCAGCAGCTGCTCCACCAGCTGGCTGCCCTAC	769
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768	LysserThrLeuserGlyValThrPheGLyLeuFrValSerGluGLyThrAlaArg	700
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222	TyrPheLeuGluTrpLeuArgLeuGluIleAlaProLysHisTyrLeuLysTrpLeuAsp	203
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02	LvsLeuArgGlvGlvProSerIleValPheAlaHisSerMetGlvAsnAsnValPheArg	183
62 52	LysteuGluGluArgAspteuTyrPheHistysteuThrPheGluThrAlateu 182AATGAAAACGGCCCTACTTCCTGGCCCTCCGCGAGATGATCGAGGAGATGTAC 552	163 499
98		442
62	GlyIleGluAlaAsnAlaIleValAlaValProTyrAspTrpArgLeuSerProThr 162	144
да .ii	TGGGTTCCTATTTCCACACCATGGTG-GAGAGCCTTGTGGGCTGG	398
9 23	123	109
40	ACAACAAAACATCCAGGGCCACCCAGTTTCCTGATGGTGTGGATGTACGTG	290
.08	ProTyrAenGlnThrAepHisProGluCysLysSer	97
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TITULE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND
FILE REFERENCE: 2456USOP
CURRENT APPLICATION NUMBER: US/09/402,532
CURRENT FILING DATE: 1999-10-04
EARLIER APPLICATION NUMBER: DT/JP98/01643
EARLIER APPLICATION NUMBER: UP 10-010289
EARLIER APPLICATION NUMBER: UP 9-184885
EARLIER APPLICATION NUMBER: UP 9-093355
EARLIER APPLICATION NUMBER: UP 9-093355
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                                                                                                                                                                     US-09-651-651-5 (1-546) x US-09-402-532-16 (1-1242)
                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 16
LENGTH: 1242
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 16, Applica Patent No. 6498019 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1159
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                                  218 CGGCTCACTACACCTCTGCCTCCCAGGCTCAAGCACTTCTCCTGCCTCAGACTC-----
                                                                59 IleLeuAspCysProTyrThrPro-----LeuAspPheAsnProLeuAspLeuValTrp 76
                                                                                                                                 39 SerLysLeuSerGlyIleIleIleProGlyPheAlaSerThrGlnLeuArgAlaTrpSer 58
77 LeuAspThrThrLysLeuLeuSerAlaValAsnCysTrpPheLysCysMetValLeuAsp 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCAGGCAGCGAG---CACATCGAGATG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ValAspGlyAsnAlaGlyProIleThrGlyAspGluThrValProTyrHisSerLeuSer 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IleIleThrAspIleIleTyrGluThrGluGlySerLeuValSerArgSerGlyThrVal 450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAGTGCCAGGCCTGGCAGAGCCGCCAGGAGCACCAAGTGTTGCTG-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGCTTTGGTGAC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGCTGGTGGAAGCCACGATGCCÁCCTGGCGTGCAGCTGCACTGCCTCTÁTGGT-----
                                                                                                      TCATTGACTGCTGGATTGACAATATCAGGCTGGAGTGCAGTG------
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22.46%
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Matches:
Conservative:
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108	pHisProGluCysLysSer	97 ProTvrAsnGlnThrAspHi	Ş	
ι, , ω	CGGATAACTGGGATTACAGGCTGGTTT-	, ,	Db 4	
sCysMetValLeuAsp 96	enasnThrThrLvsLenLenSerAlaValAsnCvsTroPheLvsCvsMetValLeuAs	77 LenAsnThrThrLvsLen	Ş	
LeuAspPheAsnProLeuAspLeuValTrp 76    :::         AAGCACTTCTCCTGCCTCAGACTC 361	AGGCTC	308 CGGCTCACTACACCTCTGCCTCCC	B 8	
nLeuArgAlaTrpSer 58	SerLysLeuSerGlyIleIleIleProGlyPheAlaSerThrGlnLeuArgAlaTrpSe 	39 SerLysLeuSerGlyIle     :::   ::: 257 TCATTGACTGCTGGATTC	QV dd	
	-402-532-18 (1-1332)	·651-5 (1-546) x US-09-402-	US-09-651-6	
	4 Length: 1332 Matches: 115 Conservative: 58 Mismatches: 154 Indels: 186 Gaps: 25	ment Scores: 2.03e-14 s: 209.00 est Similarity: 33.79* Local Similarity: 22.46* / Match: 7.05*	Alignment Spred. No.: Score: Score: Percent Sin Best Local Query Match DB:	
CGATGGTACTGAAGAGTGCCCTG 1113 CGATGGTACTGGAACTTGAAGAGTGCCCTG 1113 LASHIEThrMETAlaPrOGInPrOGINHIS 490 ::: GCACCAAGTGTTGCTGCAGGAGCTG 1167 nValAspHisGluHisGlySerAspIleIle 510	DLysVa ::: CCAGGA  :::  ::: GATG GATG TCTGAA TCTGAA TCTGAA TCTGAA TCTGAA TCTGAA TCTGAA TCTGAA TCTGAA TCTGAA TCTGAA TCTGAA TCTGAA TCTGAA	10 TIPCYSLYSASTY  71 TIPCYSLYSASTY  71 TIPCYSLYSASTY	Db 1069 T  Qy 471 T  Db 1114 C  Qy 491 A  Db 1168 C  Qy 511 A  Db 1195 G  RESULT 15  PACHENCE 18,  PACHENCE 18,  PACHENCE 18,  PACHENCE 18,  PACHENCE 18,  PACHENCE 18,  PACHENCE TILL  EARLIER FILL  EARLIER APPL  EARLIER APPL  EARLIER FILL  EARLIER FILL	
pGluThrValProTyrHisSerLeuSer 470 	pGlyAsnAlaGlyProIleThrGlyAspGluThrValPr	451 ValAspGlyAsnAlaGly	Qy 4	
SerbenvalserArgserGryintvar 350           :::	IleThrAsplieIleTyrclurnrGlUGJyserLeuvalserArgserGlyIII val 	431 IleIleThrAspIleIle .033TAC	Qу 4 Db 10	
10	ACTGGCGTCCC	} }		

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1042 GGGCTGGTGGAAGCCACGATGCCACCTGGCGTGCAGCTGCACTGCCTCTATGGT----- 1095
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                                                  431 IleIleThrAspIleIleTyrGluThrGluGlySerLeuValSerArgSerGlyThrVal 450
                                                                                                                                   411 LeuLysThrGluValGlyTyrTyrPheAlaProSerGlyLysProTyrProAspAsnTrp 430
                                                                                                                                                                                                                                                                 391 ProLeuThrProTrpGluArgProProIleLysAsnValPheCysIleTyrGlyAlaHis 410
                                                                                                                                                                                                                                                                                                                      988 TTCTTCCAGGACATCGGCTTTGAAGATGGCTGGCTCATGCGGCAGGACACA-----GAA 1041
                                                                                                                                                                                                                                                                                                                                                                           970
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          282 GlyAspAsnThrSerTrpThrHisPheSerGlyGlyAlaAlaLysLysAspLysArgVal 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          598 -----AATGAAAACGGGCCCTACTTCCTGGCCCTCCGCGAGATGATCGAGGAGATGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163 LysLeuGluGluArgAspLeuTyrPheHisLysLeuLysLeuThrPheGluThrAlaLeu 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       342 GluCysGlyLeuProThrLeuLeuSerPheThrAlaArgGluLeuAlaAspGlyThrLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LysSerThrLeuSerGlyValThrPheGlyLeuProVal---SerGluGlyThrAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlnHisIleHisAlaTyrPheAlaValGlyAlaProLeuLeuGlySerValGluAlaIle 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGCTGTATGGGGGCCCCGTGGTGCTGGTTGCCCACAGTATGGGCAACATGTACACGCTC
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:::::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PheLysAlaIleGluAspTyrAspProAspSerLysArgMetLeuHisGlnLeuLysLys 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LeuLeuSerAsnSerPheAlaSerSerLeuTrpLeuMetProPheSerLysAsnCysLys 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGCTACACACGGGGTGAGGATGTCCGAGGGGGCTCCCTATGACTGGCGCCCGAGCCCCA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGCGTCCTGGCTTCAGGAGACAACAACCGGATCCCAGTCATCGGGCCCCTGAAGATCCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                -----CTGCGGGACTAC-----CGCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AsnIleGluIleProSerThrSerValThrGluThrAlaLeuValAsnMetThrSerMet 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----CCTGAGAAGGTGTTCGTGCAGACACCCACAATCAACTACACA
----TACTATGAG-----AGCTTCCCTGACCGTGACCCTAAAATC 1158
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1285 GCCAACGCCACCCTGGCCTATCTGAAACGTGTG 1320
                                                                                                                                                                           1204 CAGTGCCAGGCCTGGCAGAGCCGCCAGGAGCACCAAGTGTTGCTG-----CAGGAGCTG 125:
                                                                                                                    491 AspGlySerAspValHisValGluLeuAsnValAspHisGluHisGlySerAspIleIle 510
                                         511 AlaAsnMetThrLysAlaProArgValLysTyrIle 522
                                                                                                                                                                                                                                                                                                       451 ValAspGlyAsnAlaGlyProIleThrGlyAspGluThrValProTyrHisSerLeuSer 470
                                                                                       CCAGGCAGCGAG --- CACATCGAGATG-----
                                                                                                                                                                                                              TrpCysLysAsnTrpLeuGlyProLysValAsnIleThrMetAlaProGlnProGluHis 490
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Search completed: November 22, 2005, 13:54:28 Job time : 237 secs

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Command line parameters:

-MODEL-frame+_p2n.model -DEV=xlh
-Q-|cgn2 1/USPTO_spool/US09651651/runat_18112005_101832_20311/app_query.fasta_1.711
-DB=publIshed_App_ications_WA_Main -QFWT=fastap -SUFFIX=rnpbm -MINMATCH=0.1
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MARRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOLALIGN=200 -THR_SCORE=pct -THR_MX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFWT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09651651_@CGN 1 797 @runat 18112005_101832_20311
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NGE_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEDUT=120 -WARN_TIMEDUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein -
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9 US-10-425-15-93909

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                  TrpThrHisPhe-----SerGlyGlyAlaAlaLysLysAspLysArgValTyrHis
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                                                                                                        Sequence 16008, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:
APPLICANT: LA Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 16008
LENGTH: 1760
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGACCCCCAATAAAGAATGTGTTCTGCATATATGGGCTTGATTCAAAGACTGAGGTAGGC
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Score:
Percent Similarity:
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
ITITLE OF INVENTION: Soy Nucleic Acid Molecul
ITITLE OF INVENTION: Plants and Uses Thereof
FILE REFERENCE: 38-21 (5323) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 134518
LENGTH: 528
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US-10-424-599-134518
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Best Local Similarity:
Query Match:
DB:
                                                  US-09-651-651-5 (1-546)
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                                                                                                                                                                                                            ORGANISM: Glycine FEATURE:
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GTCCTCCTCGCCGTGCTCGCCGGAGCCACCTCA---GACGACGGCGCGGAGCTC-----
                       ValPhePheLeuIleCysGlyGlyArgThrAlaValGluAspGluThrGluPheHisGly
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DB:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Nucleic Acid Molecules
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (53222) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 93907
LENGTH: 848
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: La Rosa, Thomas
APPLICANT: Kovalic, David
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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  TTCAACTTTCTTACGCTCATTTACATT------GCTTTCTCTGCGGTAAATTGC
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                                                                 ArgProAspSerGlyLeuSerAlaIleThrGluLeuAspProGlyTyrIleThrGlyPro
                                                                                                         TGGCTTAAATGCATGCTTGAACCCTATAATCAGATAGACCATCCCGAATGCAAGTCA
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Sequence 137717, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and PILICANT: Cao, Yongwei
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 137717
LENGTH: 924
                                                                                                        RESULT 6
US-10-425-115-93909
; Sequence 93909, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
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US-10-425-115-137717
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US-10-425-115-137717
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
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ORGANISM: Zea mays
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CURRENT FILING DATE: 2003-04-28;
NUMBER OF SEG ID NOS: 369326;
SEG ID NO 93909;
LENGTH: 1383;
TYPE: DNA
CORGANISM: Zea may8;
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_185632;
US-10-425-115-93909
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                                              aProLeuLeuGlySerVal-----GluAlaIleLysSerThrLeu
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US-10-883-760-45
; Sequence 45, Application US/10883760
; Publication No. US20050035174A1
; GENERAL INFORMATION:
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; OTHER INFORMATION: n is a,
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APPLICANT: Zhang, Hongxiang
APPLICANT: Zhang, Hongxiang
TITLE OF INVENTION: ACUTERANSFERASES FOR ALTERATION OF POLYUNSATURATED FATTY ACIDS
TITLE OF INVENTION: AND OIL CONTENT IN OLEAGINOUS YEASTS
FILE REFERENCE: C12302 US NA
CURRENT APPLICATION NUMBER: US/10/883,760
CURRENT APPLICATION NUMBER: US/10/883,760
CURRENT APPLICATION ONS: 86
SOFTWARE: Patentin version 3.2
SEQ ID NO 45
LENGTH: 2326
TYPE: DNA
ORGANISM: Yarrowia lipolytica
FEATURE:
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                            PheLeuGluTrpLeuArgLeuGluIleAlaProLysHisTyrLeuLysTrpLeuAspGln 223
                                                                                                LeuArgGlyGlyProSerIleValPheAlaHisSerMetGlyAsnAsnValPheArgTyr 203
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                                                                                                                                 Sequence 17331, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:
APPLICANT: LA ROSA Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
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    -valThrPheGlyLeuProValSerGluGly 258
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Sequence 25, Application US/10321802

Publication No. US20030200563A1

GENERAL INFORMATION:

APPLICANT: Butler, Karlene H.

APPLICANT: Cahoon, Edgar B.

APPLICANT: Cahoon, Rebecca E.

APPLICANT: Famedu, Omolayo O.

APPLICANT: Hall, Sarah E.

ITILE OF INVENTION: Phopholipid:diacylglycerol Acetyltransferases

FILE REFERENCE: BB1486 US NA

CURRENT APPLICATION NUMBER: US/10/321,802

CURRENT FILING DATE: 2002-12-17

NUMBER OF SEQ ID NOS: 36

SOFTWARE: Microsoft Office 97

SEQ ID NO 25

ITMOREMENT STANDAMENT OF SERVICE STANDAMENT OF SEQ ID NO 25
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_115655C.1
US-10-424-599-17331
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US-10-321-802-25
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Alignment Scores: Pred. No.:
                                                     US-10-321-802-25
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 17331
LENGTH: 1433
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LOCATION: (1)..(1433)
OTHER INFORMATION: unsure at all n locations
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ORGANISM: Glycine
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TYPE: DNA
ORGANISM: Helianthus
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                                                                                                                                    rPheGlyLeuProValSerGluGlyThrAlaArgLeuLeuSerAsnSerPheAlaSerSe 270
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RESULT 10
US-10-321-802-23
US-10-321-802-23
Sequence 23, Application US/10321802
Publication No. US20030200563A1
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  GENERAL INFORMATION:
APPLICANT: Butler, Karlene H.
APPLICANT: Cahoon, Edgar B.
APPLICANT: Cahoon, Rebecca E
APPLICANT: Famodu, Omolayo O
APPLICANT: Hall, Sarah E.
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Cahoon, Edgar B.
Cahoon, Rebecca E.
Famodu, Omolayo O.
Hall, Sarah E.
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FILE REFERENCE: BB1486 US NA
CURRENT APPLICATION NUMBER: US/10/321,802
CURRENT FILING DATE: 2002-12-17
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Microsoft Office 97
SEQ ID NO 23
LENGTH: 2700
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        ACCTTGCAACATGTAATGAAGATGACCCGTACTTGGGACTCAACAATGTCAATGATACCA 1406
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ORGANISM: Triticum aestivum
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                                       ATTTGGGGAGGTTTGGATTGGTCTCCAGAAGATGGTTTTGAGTGTAAATCCAAGAAGCGG
                                                                                                                                                                                             GCTATTGCACCAGAAATGCTGGACTCAGATTTTCTTGGACTTCAGACCTTGCGCCACTTG
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¿ Sequence 17, Application US/10321802
; Publication No. US20030200563A1
; GENERAL INFORMATION:
         APPLICANT: Buller, Karlene H.
APPLICANT: Cahoon, Edgar B.
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Famodu, Omolayo O.
APPLICANT: Famodu, Omolayo O.
APPLICANT: Hall, Sarah E.
TITLE OF INVENTION: Phopholipid:diacylglycerol Acetyltransferases
FILE REFERENCE: BB1486 US NA
CURRENT APPLICATION NUMBER: US/10/321,802
CURRENT APPLICATION NUMBER: US/10/321,802
CURRENT FILING DATE: 2002-12-17
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Microsoft Office 97
SEQ ID NO 17
LENGTH: 2479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCTACAAATGGTGGGAAAAAGGCGGTTATTATCCCACATTCAATGGGTGTTATCTACTTC
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                                       AlaAlaLysLysAspLysArgValTyrHisCysAspGluGluGluTyrGlnSerLysTyr 313
                                                                                                                                                                            ATAATGAGA---ATGAGCCGCACATGGGATTCAACCATGTCTATGATACCA-----
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US-10-437-963-38278/c
; Sequence 38278, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
: APPLICANT: La Rosa, Thomas J.
: APPLICANT: Kovalic, David K.
: APPLICANT: Zhou, Yihua
: APPLICANT: Cao, Yongwei
: APPLICANT: Boukharov, Andrey A.
: APPLICANT: Boukharov, Andrey A.
: APPLICANT: Boukharov, Brad
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US-09-651-651-5 (1-546) x US-10-437-963-38278 (1-2395)
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT FILLIS DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 38278
LENGTH: 2395
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2017 GTGTTCGTCCCGGGCATCGTCACCGGCGGCCTCGAGCTCTGGGAGGGGCACCAGTGCGCC
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241 AlaIleLysSerThrLeuSerGlyValThrPheGlyLeuProValSerGluGlyThrAla
                                                                                                                                                                                                                         206 GluTrpLeuArgLeuGluIleAlaProLysHisTyr------LeuLysTrp 220
                                                                                                                                                                                                                                                                                                                          GlyproSer---IleValPheAlaHisSerMetGlyAsnAsnValPheArgTyrPheLeu 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAAAAGACCATGTACATGGCTGCATATGATTGGAGGTTATCTTTCCAGAACACTGAGGTT 1619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AlaAsnAlaIleValAlaValProTyrAspTrpArgLeuSerProThrLysLeuGluGlu 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LysSerArgProAspSerGlyLeuSerAlaIleThrGluLeuAspProGlyTyrIleThr 126
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                                                                                                         LeuAspGlnHisIleHisAlaTyrPheAlaValGlyAlaProLeuLeuGlySerValGlu
                                                                                                                                                                                                                                                                                                                                                                                                   CGTGATCAAACTTTGAGCAGGATAAAAAGTAACATTGAACTCCTGGTAGCAACTAATGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GlyProLeuSerThrValTrpLysGluTrpLeuLysTrpCysValGluPheGlyIleGlu 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGAGTTCGGCCAGTCACAGGCCTAGTGGCAGCAGACTATTTTGTTCCTGGGTATTTT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PheAsnProLeuAspLeuValTrpLeuAsp-----ThrThrLysLeuLeuSerAlaVal 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----ProTyrThrProLeuAsp 68
                                                             TGTGCAAAGCACATCAAATCTGTAATGAATATTGGCGGACCTTTCTTAGGAGTTCCTAAG
                                                                                                                                                                          AAGTGGGTTGAG------GCTCCTCCTCCCATGGGTGGTGGTGGTCCAAATTGG
                                                                                                                                                                                                                                                                                   GGAAATAGGGTGGTGATCCCACATTCTATGGGGGTTCTCTATTTTCTGCATTTTATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GATTTGGATTGGTCTCCAGAAGATGGTTTTGAGTGTAAAAGCTAAGAATCAGAAAATC--- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTCCATTATAGATCTTCTTCGTTTTGTTGCTCCAAGGATGATGCAGCGTGGAAGTGTTCA 798
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pSerGluSerIleProGlyLysArgThrAlaValTrpGluLeu 541
                                                                                        rAspilelleAlaAsnMetThrLysAlaProArgValLysTyrileThrPheTyrGluAs 527
                                                                                                                                                                                                                                   TTCTGGCAGCAAGACCTACGTCAGAGAATACAGCCATTCTCCACCCTCAAATCTCCTCGA
                                              -GATATCATGGGGAATTTTGCTTTAATCGAGGATATTATCAGGATTGCTGCTGGGGCAAC
                                                                                                                                                                                 --GlySerAspValHisValGluLeuAsnValAspHisGluHisGlySe 507
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DB:
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Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
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    211 GluIleAlaProLysHisTyr----
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                                                                                                                                                                                                                                                                                    AlaValProTyrAspTrpArgLeuSerProThrLysLeuGluGluArgAspLeuTyrPhe 171
                                                                                                                                                                                                                                                                                                                                                                                                                                 ACAGGCCTGGTTGCAGCAGACTATTTTGTCCCTGGATATTTT---------
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                                                 ValTrpLysGluTrpLeuLysTrpCysValGluPheGlyIleGluAlaAsnAlaIleVal 151
                                                                                                                                                                                                                                          ATGGCTGCATATGATTGGAGGTTATCTTTCCAGAACACTGAGGTCCGTGATCAAACTTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     376 LeuHisGlnLeuLysLysLeuTyrHis------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    314 SerGly-----TrpProThrAsnIleIleAsnIleGluIleProSerThrSerValThr 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             274 MetProPheSerLysAsnCysLysGlyAspAsnThrSerTrpThrHisPheSerGlyGly 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          226 HisAlaTyrPheAlaValGlyAlaProLeuLeuGlySerValGluAlaIleLysSerThr 245
                                           492
                                                                                                                                                                                                                                                                                       ThrGlyAspGluThrValProTyrHisSerLeuSerTrp-----CysLy8AsnTrpLeu 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTCTCATCTGAAGCCAAAGATGTTGCCGTTGCTAGAGCTATCGCTCCTGATGTCTTGGAC 1208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAAGCTGTAATGAATATTGGAGGACCTTTCTTAGGAGTTCCTAAGGCTGTTGCTGGCCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTGGCCCCACAGGCAGAATGTTAT------ATACCTTTCCGAATTGACACCTCG 1904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LysAsnValPheCysIleTyrGlyAlaHisLeuLysThrGluValGlyTyrTyrPhe----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGGGAGATCTGGACAGAGTATCACGAATTAGGATGGGGTGGAATAAAGGCAGTCGCAGAC 1616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GluThrAlaLeuValAsnMetThrSerMetGluCysGlyLeuProThrLeuLeuSer--- 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGGATTGGTCTCCAGAAGATGGCATTGAATGTAAAGCTAAGAAGCAAAAGCCAATGAT 1376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCAACAATTTCAATGATTCCTAAAGGTGGTGATACAATTTGG------GGAAAT 1316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AsnSerPhe-----AlaSerSerLeuTrpLeu 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LeuSerGlyValThrPheGlyLeuProValSerGluGlyThrAla---ArgLeuLeuSer 264
                                                                                                                                                                                                                                                                                                                                                                                                                                           ThrGluGlySerLeuValSerArgSerGlyThrValValAspGlyAsnAlaGlyProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAGATAGAATTTCGTGATGCTGTTAAAGGTAATAATATCGCCCATTCAAATACGTCATGC 1556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TATGGAAGGCTGGTATCTTTTGGTAAAGATGTAGCAGAAGCACCTTCTTCAGAGAGTGAG 1496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTGGGGTTTCTAAGGATAGCAATGGGGGAAATATCGAGGTTCAACCTGAACCTATTAAC 1436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AlaAlaLysLysAspLysArgValTyrHisCysAspGluGluGluTyrGlnSerLysTyr 313
                                                                                                        GGCAAAACTCGTTTCAACCCTGCCGGCAGCAAGACTTACGTGAGAGAATACAGCCATTCA 2075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---AlaProSerGlyLysProTyrProAspAsnTrpIleIleThrAspIleIleTyrGlu 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGCAGCGTGGAAATGTTCACTTTTCATATGGAATTGCTGATAACTTGGATGATCCGAAA 1736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---PheThrAlaArgGluLeuAlaAspGlyThrLeu----------
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----GlySerAspValHisValGluLeuAsn 500
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Publication No. US20030200563A1

GENERAL INFORMATION:
APPLICANT: Butler, Karlene H.
APPLICANT: Cahoon, Edgar B.
APPLICANT: Cahoon, Edgar B.
APPLICANT: Famedu, Omolayo O.
APPLICANT: Hall, Sarah E.
TITLE OF INVENTION: Phopholipid:diacylglycerol Acetyltransferases
FILE REFERENCE: Balt486 US NA
CURRENT APPLICATION NUMBER: US/10/321,802

CURRENT FILING DATE: 2002-12-17
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Microsoft Office 97
LENGTH. AGGS

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Query Match:
DB:
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US-10-321-802-35
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       945
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                                                                                                                                                                                                                                                                                                                                                                                                                            783
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           615 GTTTTTGTGCCCGGGATTGTCACTGGGGGGCTTGAACTGTGGGAGGGTCACCTGTGTGCT
                                                                    163 LysLeuGluGluArgAspLeuTyrPheHisLysLeuLysLeuThrPheGluThrAlaLeu 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83 LeuSerAlaValAsnCysTrpPheLysCysMetValLeuAspProTyrAsnGlnThrAsp 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44 IleIleIleProGlyPheAlaSerThrGlnLeuArgAlaTrpSerIleLeuAspCysPro 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TyrThrProLeuAspPheAsnProLeuAspLeuValTrpLeuAspThr----ThrLysLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :::||||||:::
TTGTAACCTATGGGAAGTT 2274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sAlaProArgValLysTyrIleThrPheTyrGluAspSerGluSerIleProGlyLysAr 535
          AACACTGAGGTGAGGGATCAAACACTAAGTCGGATAAAAAGCAACATAGAACTTATGGTT 1004
                                                                                                                                           ATTGGTTATGAAGAAAAACTATGTACATGGCTGCATATGATTGGAGAATAGCATTTCAG 944
                                                                                                                                                                                          PheGlyIleGluAlaAsnAlaIleValAlaValProTyrAspTrpArgLeuSerProThr 162
                                                                                                                                                                                                                                                                                                                                          GlyTyrIleThrGlyProLeuSerThrValTrpLysGluTrpLeuLysTrpCysValGlu 142
                                                                                                                                                                                                                                                                                                                                                                                                                            CCACCAGGGATAAGAGTTAGGCCTGTCTCTGGACTTGTAGCTGCTGATTACTTTGCTGCA 842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TATAAAAGACCTTCATGCTGGGTGGATCACATGTCACTGGACAATGAAACAGGATTGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGGGGTTGTTC-----AGGAAACGCTTATGGGGTGGTACCTTCGGAGAAGTT
                                                                                                                                                                                                                                                                                GGATACTTT------GTATGGGCAGTGCTAATTGCTAACTTGGCACGC 884
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGAACTTTGCTCTAATTGAGGACGTCATCAGAATAGCTGCTGGGGCAACCGGTGAGGAA
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Search completed: November 22, 2005, 14:08:37 Job time : 866 secs

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Minimum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -MODEL-frame+_D2n.model DBV=xlh
-Q=/Cgn2 1/USPTO_spool/US09651651/runat_18112005_101832_20333/app_query.fasta_1.711
-Q=/Cgn2 1/USPTO_spool/US09651651/runat_18112005_T01832_20333/app_query.fasta_1.711
-DB=Published_Applications_NA_New--OFMT=fastap_-SUFFIX=rnpbn -MINMATCH=0.1
-DOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DCALICS=200 -TRR_SCORE=pct -THR_MAX=100
-TRANS=human40.cdi -LIST=45 -DCALICS=200 -TRR_SCORE=pct -THR_MAX=100
-TRANS=human40.cdi -LIST=45 -DCALICS=200 -TRR_SCORE=500 -MINLEN=0
-TRANS=human40.cdi -LIST=45 -DCTALICS=200 -NORM=ext -HEAPSIZE=500 -MINLEN=0
-TRANS=15 -MODEL-15 -MODEL-LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXIEN=200000000 -USER=US09651651_@CGN 1 117_@runat 18112005_101832_20333
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -MAIT -DSPBLOCK=100
-NORUCGG -DUY TIMEDUT=30 -THREDUT=30 -THREADS=1 -XCARPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGĀPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Command line parameters:
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                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being pu and is derived by analysis of the total score distribution.
                                                                                                                                   104
                                                                                                                                                                                                      Score
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seq length: 2000000000

    nucleic search, using frame_plus_p2n model

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1: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*

2: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

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6: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*

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## ALIGNMENTS

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US-10-131-826A-233
; Sequence 233, Application US/10131826A
; Publication No. US20050245730A1
; General INFORMATION:
    APPLICANT: Baker, Kevin P.
    APPLICANT: Beresini, Maureen
    APPLICANT: Desorge, Laura
    APPLICANT: Desorge, Laura
    APPLICANT: Desorge, Laura
    APPLICANT: Desorge, Laura
    APPLICANT: Geodwski, Paul J.
    APPLICANT: Goddard, Audrey
    APPLICANT: Goddwski, Paul J.
    APPLICANT: Sherwood, Steven
    APPLICANT: Sherwood, Steven
    APPLICANT: Sherwood, Steven
    APPLICANT: Sherwood, Steven
    APPLICANT: Wood, William
    APPLICANT: Wood, William
    APPLICANT: Watanabe, Colin K
    APPLICANT: Shermood, SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: SCIENCED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
    FILE REFERENCE: P3330RIC138
    CURRENT APPLICATION NUMBER: US/10/131,826A
    CURRENT FILING DATE: 2002-04-24
    PRIOR APPLICATION NUMBER: 60/056974
    PRIOR APPLICATION NUMBER: 60/056974
    PRIOR APPLICATION NUMBER: 60/059113
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FILING DATE:

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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330RICL28 CURRENT APPLICATION NUMBER: US/10/131,826A CURRENT FILING DATE: 2002-04-24 PRIOR APPLICATION NUMBER: 60/049911 PRIOR APPLICATION NUMBER: 60/049911 PRIOR FILING DATE: 1997-06-18 PRIOR FILING DATE: 1997-08-26 PRIOR APPLICATION NUMBER: 60/059113 PRIOR APPLICATION NUMBER: 60/059113 PRIOR APPLICATION NUMBER: 60/059115 PRIOR APPLICATION NUMBER: 60/059115 PRIOR APPLICATION NUMBER: 60/059115 PRIOR APPLICATION NUMBER: 60/059117 PRIOR APPLICATION PRIOR APPLICATION NUMBER: 60/059117 PRIOR APPLICATION NUMBER: 60/059117 PRIOR APPLICATION NUMBER: 60/059117 PRIOR APPLICATION NUM
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PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR APPLICATION NUMBER: 60/059352
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                                                                                                                                                                                                      Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 550
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LENGTH: 2806
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                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 1997-09-19
                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
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NAME/KEY: unsure
LOCATION: 2157
OTHER INFORMATION: unknown base
                                                                                                                                          TYPE: DNA
ORGANISM: Homo Sapien
                                                                                                              FEATURE:
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Watanabe, Colin K
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                                                                      APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C128
CURRENT APPLICATION NUMBER: U5/10/131,826A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/049911
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-06-18
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR APPLICATION NUMBER: 60/059115
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                   FILING DATE: 1997-09-17
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; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
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; SEQ ID NO 367
; LENGTH: 2906
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                                                                                                                                                                                                                                                                                                                                                                               gProProIleLysAsnValPheCysIleTyrGlyAlaHisLeuLysThrGluValGlyTy 417
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                                                                                                                                                                                                                                        CCAGCCAGCAGGCCCGTGGCCTGGAGGGCAGCCGATGTAGTTGCGAGGCCTCTGGCCCGC 482
                                                                                                                                                                                                                                                                                                                                CCCCTACATCAAGGTACCTGGGTGCCCCCAGGGCTCA---GCCACAGCCAAGGTGGGATT 4768
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rLeuSerTrpCysLysAsnTrpLeuGlyProLysValAsnIleThrMet----AlaProGl 487
                                                                                                                                              GCGCTGGGGGCTG--
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                                                                                                                                                                                                                                                                                  rTyrPheAla-----ProSerGlyLysPro-----
                                                 GGGTGATCTTCTGGGCGGAGGAGCAGAATATACGGGG-
                                                                                             YThrValValAspGlyAsnAlaGlyProIleThrGlyAspGluThrValProTyrHisSe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCTCGGGCTGGGCCTCCTGCAAGGAGACCTTCACCGT 465:
                                                                                                                                                - GAAGCAGGAGGCTTAGGTCTGGGGAGGGAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-651-651-5 (1-546) x US-10-647-956A-7 (1-7512)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: DNA SEQUENCES FROM PHOTORHABDUS LUMINESCENS FILE REFERENCE: 61645
CURRENT APPLICATION NUMBER: US/10/647,956A
CURRENT FILING DATE: 2003-08-26
PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/817,514
PRIOR FILING DATE: CURRENT FILING DATE: 2000-03-26
PRIOR APPLICATION NUMBER: US 60/191806
PRIOR APPLICATION NUMBER: US 60/191806
PRIOR APPLICATION DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 8
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TYPE: DNA
ORGANISM: Photorhabdus luminescens
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         2686 GGGATAGATCATAACTATGCTGCCTGGCAAGCTGCGGCGGCTGCGCCTGATGGCTGATCAT 2745
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                                                                                                                                                                                                                                                                                                                                     TyrPheHisLysLeuLysLeuThrPheGluThrAlaLeuLysLeuArgGlyGlyProSer 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCTCCTTGATATTGGCGGCGTTGAAAGACGGAGCCTTGACAGTTACCGATGTAGCACAA 2514
                                                                                                  ATGTCTTCGGCCTTGGCGGTTTCTCCACTGGATCTGGCAGGGATGATGGCCCTGAAATAT 2689
                                                                                                                                                                                                                                      IleValPheAlaHisSerMetGlyAsnAsnValPheArgTyrPheLeuGluTrpLeuArg 209
                                                   ---LeuAspGlnHisIleHisAlaTyrPheAlaValGlyAlaProLeuLeuGlySer---
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Matches:
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RESULT 6
US-11-147-725-3
; Sequence 3, Application US/11147725
; Publication No. US20050244878A1
; GENERAL INFORMATION:
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              Percent Similarity:
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Query Match:
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                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 10/026,140
PRIOR FILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1455
TYPE: DNA
ORGANISM: Trichoderma reesei
                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Dunn-Coleman, Nigel
APPLICANT: Goedegebuur, Frits
APPLICANT: Ward, Michael
APPLICANT: Ward, Michael
TITLE OF INVENTION: BGL5 Beta-Glucosidase
TITLE OF INVENTION: Encoding the Same
FILE REFERENCE: GC697
                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE: 2005-06-07
                                                                                                        No.:
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                                                                                                                                                                                                                                                                                                                       Leu---ThrProTrpGluArg-----ProProIle-----LysAsnValPheCysIle
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                                 GlyAsnAlaGlyProIleThrGlyAspGluThrValProTyrHisSerLeuSerTrpCys 472
                                                                                                        ---AspIleIleTyrGluThrGluGlySerLeuValSerArgSerGlyThrValValAsp
                                                                                                                                          CCTGGAGAGAGAACATGACGTGCGAGGAGGCCGTCAACGACCCCTTCCGCATCCGSTAC 122
                                                                                                                                                                         ProAspAsnTrpIleIleThr------
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                                                                                                                                                                                                                                                                                                                                                           TATCTCGGCGCCATCCATGAGCACCAGGAGAATAAGGACGGCAGCCCCGTTGGCGAGGAG
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-----AACTTGGAATGGTCA 1326
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; ORGANISM: Trichoderma
US-11-147-725-1
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LENGTH: 1991
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CURRENT APPLICATION NUMBER: US/11/147,725
CURRENT FILING DATE: 2005-06-07
PRIOR APPLICATION NUMBER: US 10/026,140
PRIOR FILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for Windows Version 4.0
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TITLE OF INVENTION: BGL5 Beta-Glucosidase and
TITLE OF INVENTION: Encoding the Same
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GluGluTyrGlnSerLysTyrSerGlyTrpProThrAsnIleIleAsnIleGlu-----
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                                                                                                   TACAGCAGGGACTTTCGCCCCTCGCAAAAGGGCCAGATCGGCATCTCGCTCAACGGCGAC
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                                            TACTATGAGCCCTGGGACAGCAATGAGCCTCGGGACAAGGAGGCT------
                                                                      TrpThrHisPheSerGlyGlyAlaAlaLysLysAspLysArgValTyrHisCysAspGlu
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TITLE OF INVENTION: PROMOTER, PROMOTER CONTI-
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 2750-1577PUS3
CURRENT APPLICATION NUMBER: US/10/957,569
CURRENT FILING DATE: 2004-09-30
PRIOR APPLICATION NUMBER: US 10/950,321
PRIOR FILING DATE: 2004-09-23
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn version 3.3
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                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Arabidopsis thaliana
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APPLICANT: Plesch, Gunnar
APPLICANT: Blau, Astrid
APPLICANT: Blau, Astrid
APPLICANT: Klein, Mathieu
TITLE OF INVENTION: Identification of Herbicidally Active Sub
FILE REFERENCE: 2000 165
CURRENT APPLICATION NUMBER: US/10/467,962B
CURRENT FILING DATE: 2003-08-14
PRIOR APPLICATION NUMBER: PCT/EP02/01466
PRIOR APPLICATION POSSIBLE PCT/EP02/01466
                                                                                                                                                                                                                                                                                                                                    RESULT 9
US-10-467-962B-78
                                                                                                                                                                                                                                                                   Sequence 78, Application US/10467962B Publication No. US20050246784A1 GENERAL INFORMATION:
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, NAME/KEY: CDS
, LOCATION: (1)...(1023)
, OTHER INFORMATION: ORF
US-10-467-962B-78
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LENGTH: 1023
TYPE: DNA
ORGANISM: Arabidopsis thaliana
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                                                    AACGAGAGCTCATGGCGATACCTA---
                                                                                         AspAsnThrSerTrpThrHisPheSerGlyGlyAlaAlaLysLysAspLysArgValTyr
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                                                                                                                                     TTAACCAAT-----
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                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn version 3.1 SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: SONN:064US
CURRENT APPLICATION NUMBER: US/10/518,599
CURRENT FILING DATE: 2004-12-17
PRIOR APPLICATION NUMBER: PCT/CA03/00882
PRIOR FILING DATE: 2003-06-19
                                                                                                                                                                                                                                                                                                                                                       LENGTH: 2739
TYPE: DNA
ORGANISM: Mus 1
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APPLICANT: CRACKOWER, MICHAEL A.
TITLE OF INVENTION: ACE2 ACTIVATION FOR TREATMENT OF HEART, LUNG AND
TITLE OF INVENTION: KIDNEY DISEASE AND HYPERTENSION
                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/389,709
PRIOR FILING DATE: 2002-06-19
NUMBER OF SEQ ID NOS: 24
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                    AspGluGluGluTyrGlnSerLysTyrSerGlyTrpProThrAsnIleIleAsnIleGlu 324
                                                                          ThrSerTrpThrHisPheSerGlyGlyAlaAlaLysLysAspLysArgValTyrHisCys
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Sequence 10, Application US/11042988 Publication No. US20050244818A1 GENERAL INFORMATION:
                                                                                                                                                                        APPLICANT: ZHOU, YAN
APPLICANT: ZHOU, YAN
TITLE OF INVENTION: SINGLE CELL ANALYSIS OF HIV REPLICATION CAPACITY AND
TITLE OF INVENTION: DRUG RESISTANCE
FILE REFERENCE: 62760(71699)
CURRENT APPLICATION NUMBER: US/11/042,988
CURRENT FILING DATE: 2005-01-25
PRIOR APPLICATION NUMBER: 60/540,716
PRIOR FILING DATE: 2004-01-30
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: SILICIANO, ROBERT
APPLICANT: ZHANG, HAILI
APPLICANT: ZHOU, YAN
                                                                                                                                                     NUMBER OF SEQ ID NOS: 16
LENGTH: 9719
TYPE: DNA
ORGANISM: Human immunodeficiency virus type
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Qy 240 Gluaria Leuysber Introduser of yadinin Friedry Medicine (1971)  Db 1870 AGAGTTTTGGCTGAAGCAATGAGCCAAGTAACAAATTCAGCTACC 1914  Qy 260 AlaargLeuLeuSerAsnSerPheAlaSerSerLeuTrpLeuMetPro	187 1651 207 2696 220 1756 221 1816	103 HisPro	US-11-042-988-10  Alignment Scores:
Oy 170 TyrPheHisLysLeuLysLeuThrPhe-GluThrAlaLeuLysLeuArg	Alignment Scores: 2.12e+05   Length: 48763 Pred. No.: 77.50   Matches: 98 Score: 77.50   Matches: 98 Score: 29.11%   Conservative: 63 Best Local Similarity: 17.72%   Mismatches: 165 Query Match: 1   Gaps: 230 DB: 1   Gaps: 22  US-09-651-651-5 (1-546) x US-10-663-794-3 (1-48763)  Qy 130 SerThrValTrpLysGluTrpLeuLysTrpCysValGluPheGlyIleGluAlaAsnAla 149	RESULT 12 US-10-663-794-3/c (Sequence 3, Application US/10663794)  Publication No. US20050244833A1  Publication No. US2005024833A1  GENERAL INFORMATION: APPLICANT: WEI, Ming-Hui et al.  TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES TITLE OF INVENTION: THEREOF FILE REFERENCE: CL001164CIP-DIV II CURRENT APPLICATION NUMBER: US/10/663,794 CURRENT FILING DATE: 2003-09-17 NUMBER OF SEQ ID NOS: 6 SOCTWARE: FASTSEQ for Windows Version 4.0 SEQ ID NO 3 LENGTH: 48763 TYPE: DNA ORGANISM: Homo sapiens US-10-663-794-3	Db 2008GCCCCTAGGAAAAAGGCTGTTGGAAATGTTGGAAAGGACACCAA 2055  Qy 311 SerLys

Db 412 GATAAAGCTTCAAGAATAGGTATTCGCGTTTGTGAT	SerTrpCysLysAsnTrpLeuGlyProLysValAsnIleThrMetAla
165 Glu	453 lyAsnAlaGlyProIleThrGlyAspGluThrValProTyrHisSerLeu 469 
Qy 159 Db 352 GAAGCTAAGGGTAAAAATAAGATTGGTACTAAG	19228
145 IleGluAlaA     292 ATTTCTAACC	
Percent Similarity: 34.08% Conservativ Best Local Similarity: 19.61% Mismatches: Query Match: 2.60% Indels: DB: 7 Gaps: US-09-651-651-5 (1-546) x US-11-074-176-247 (1-128)	19331 GGCGC
074-176-247 ent Scores: 1.38e+03 No.:	353 laArgGluLeuAlaAspGlyThrLeuPheLysAlalleGluAspTyrAspProAspSert 373 ::
; TYPE: DNA ; ORGANISM: Lactobacillus acidophilus ; FEATURE: ; NAME/KEY: CDS	316 rpProThrAsnIleIleAsnIleGluIleProSerThrSerValThrGluThrAlaLeuV 336
NUMBER OF SEQ ID NOS: 381 SOFTWARE: FASESEQ for Windows Version 4.0 SEQ ID NO 247 LENGTH: 1287	296 ysLysAspLysArgValTyrHisCysAspGluGluGluTyrGlnSerLysTyrSerGlyT 316 
	277 erLysAsnCysLysGlyAspAsnThrSerTrpThrHisPheSerGlyGlyAlaAlaL 296 
Peri NVENTI NVENTI	272TrpLeuMetProPheS 277
; APPLICANT: Klaenhammer, Todd R. ; APPLICANT: Russell, William M. ; APPLICANT: Altermann, Eric ; APPLICANT: McAuliffe, Olivia	271 eu
074-176-2 ence 247, ication N	257GluGlyThrAlaArgLeuLeuSerAenSerPheAlaSerSerL 271
Qy 517 roArgValLysTyrIleThrPheTyrGluAspSer :::    :::           ::: Db 18897 AAGCTGCACGGTATTT-TCCTTTTACCCTGACAAT	erGlyValThrPheGlyLeuProValSer
Qy 498GluLeuAsnValAspHisGluHisGlySerAspI :::     :::	erValGluAlaIleLysSerThrLeus erValGluAlaIleLysSerThrLeus erValGluAlaIleLysSerThrLeus er
Qy 486ProGlnProGluHisAspGlySerAspV ::    ::    pb 19011 GGTCCCTTGGGGAACCAGGCAAGAGTGGTGGGTGGA	20002 ATCCCAAACACACACACTGGAATCTTCTGGGAAGTGGGATGGCATTTCAATGGCTGG 13793  222 spGlnHisIleHisAlaTyrPheAlaValGlyAlaProLeuLeuGlyS 238  223 spGlnHisIleHisAlaTyrPheAlaValGlyAlaProLeuLeuGlyS 238  224 spGln
Qy 485Db 19071 TCTTCTCAGCCACAGACCCCACCCCTCACTTCAGCA	213 laProLysHisTyrLeuLysTrpLeuA
Db 19131 ACGGGTGGAGTTGAAATCTCCTGTGTCAGAGGCTTA	205LeuGluTrp

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		159 352	B &
IleGluAlaAsnAlaIleValAlaValProTyrAspTrpArg		145 292	용 성
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1.38e+03 Length: 1287 77.00 Matches: 61 77.08 Conservative: 45 arity: 19.61% Mismatches: 115 2.60% Indels: 90 7 Gaps: 16	tt Scores: .: Similarity: al Similarity: tch:	mer nt No	Align Pred. Score Perce Best : Query DB:
sc feature )).T.(0) MATION: ORF 1892; adenylosuccinate synthase	misc_f (0) ORMATIO	NAME/K LOCATI OTHER 11-074-	us-
) .) (1287)	CDS (1)	NAME/KEY: LOCATION:	
Lactobacillus acidophilus		TYPE: DNA ORGANISM:	
COLX FOR THE SECTION OF THE SECTION	47	SEQ ID NO 2	
ATE: 2004-03-08 ID NOS: 381 SED for windows Vers	SEQ ID NO	PRIOR FILII NUMBER OF S	
		CURRENT API	
ION: Nuclei		TITLE OF INVENT	
<del>- +</del>	Alterman McAulifi	APPLICANT: APPLICANT: APPLICANT:	
No. US20050250135A1  RMATION: RIGHTION: RIGHTI	_ x z z ·	Publication GENERAL INFO APPLICANT:	
7 Application US/11074176		RESULT 13 US-11-074-176-2 : Seguence 247.	RES
AAGCTGCACGGTATTT-TCCTTTTACCCTGACAAT 18864		18897	멍
roArgValLysTyrIleThrPheTyrGluAspSer 528	roArgValI	517	5
GluLeuAbnValAbpHisGluHisGlySerAbpIleIleAlaAsnMetThrLysAlaP 517 	GluLeuz ::: AAAAAACAZ	498 18951	g &
GGTCCCTTGGGGAACCAGGCAAGAGTGGTGGGTGGATCCACATGAAGTCGTGACCACTGT 18952	GGTCCCTTC	19011	дb
ProGlnProGluHisAspGlySerAspValHisVal 497	F	486	Ş
TCTTCTCAGCCACAGACCCCACCCCTCACTTCAGCAATCATCCTGAATACACCTTCCCCTT 19012	TCTTCTCAC	19071	ф
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APPLICANT: DUBENSKY, Thomas W., Jr.
APPLICANT: PORTNOY, Daniel A.
APPLICANT: LUCKETT, William S., Jr.
APPLICANT: LUCKETT, William S., Jr.
APPLICANT: COOK, David N.
TITLE OF INVENTION: RECOMBINANT NUCLEIC ACID MOLECULES,
TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, F.
TITLE OF INVENTION: TERREOF
FILE REFERENCE: 282172003900
CURRENT APPLICATION NUMBER: US/11/021,441
CURRENT APPLICATION NUMBER: US 60/616,750
PRIOR APPLICATION NUMBER: US 60/615,287
PRIOR APPLICATION NUMBER: US 60/615,287
PRIOR APPLICATION NUMBER: US 60/615,287
PRIOR APPLICATION NUMBER: US 60/599,377
PRIOR APPLICATION NUMBER: US 60/599,377
PRIOR APPLICATION NUMBER: US 60/599,377
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US-11-021-441-8
(S-11-021-441-8); Sequence 8, Application US/11021441
Publication No. US20050249748A1
GENERAL INFORMATION:
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PRIOR FILING DATE: 2004-07-23
PRIOR PPLICATION NUMBER: US 10/883,599
PRIOR FILING DATE: 2004-06-30
PRIOR APPLICATION NUMBER: US 60/556,744
PRIOR FILING DATE: 2004-03-26
NUMBER OF SEQ ID NOS: 129
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity:
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  Sequence 1, Application US/11085864
Publication No. US20050246787A1
GENERAL INFORMATION:
APPLICANT: STREATFIELD, STEPHEN J.
APPLICANT: LOVE, ROBERT T.
APPLICANT: BRAY, JEFF
TITLE OF INVENTION: A GLOBULIN-1 REGULATORY REGION FILE REFERENCE: AB0002
CURRENT APPLICATION NUMBER: US/11/085,864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1689
TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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Percent Similarity:
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PRIOR APPLICATION NUMBER: 60/555,720
PRIOR FILING DATE: 2004-03-23
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 3.3
SEQ ID NO 1
LENGTH: 1824
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ORGANISM: Artificial Sequence
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 ProLysHisTyrLeuLysTrpLeuAspGlnHisIleHisAlaTyrPheAlaValGlyAla 233
                                                                                                            ArgGlyGlyProSerIle------ValPheAlaHisSer-----
                                                                                                                                          TGGAAGTAAGACTGCTTTTTC------TTGCCGTTTTCGTCGGTAATCACCATT 438
                                                                                                                                                                ------AspLeuTyrPheHisLysLeuLysLeuThrPheGluThrAlaLeuLysLeu 184
                                                                                                                                                                                                                         AsnAlaIleValAlaValProTyrAspTrpArgLeuSerProThrLysLeuGluGluArg
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                                            ---MetGlyAsnAsnValPheArgTyrPhe---LeuGluTrpLeuArgLeuGluIleAla
                                                                                   CCCGGCGGGAT-AGTCTGCCAGTTCAGTTCGTTCACACACAAACGGTGATACGTACACT
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Search completed: November 22, 2005, 14:11:21 Job time : 186 secs

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Command line parameters:

-MODEL=frame+ D2n.model -DEV=xlh
-O=/cgn2 1/USPTO spool/US9651651/runat 18112005 101831 20261/app_query.fasta_1.711
-O=/cgn2 1/USPTO spool/US9651651/runat 18112005 101831 20261/app_query.fasta_1.711
-DB=EST -OFMT=fastap -SUFFIX=rst -MINNATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosun62 -TRANS=human40.cdi -LIST=45
-DCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09651651 @CGN 1 1 4015 @TUNAT 18112005 101831 20261 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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## ALIGNMENTS

FEATURES source	JOURNAL COMMENT	TITLE	REFERENCE AUTHORS	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	z
Department of Brownics Beijing Institute of Genomics Chinese Academy of Sciences, Beijing 101300, China Tel: 86-10-80488559 Fax: 86-10-80488576 Email: chenchen@genomics.org.cn Rice genomic sequence. Class: exon-trapped. Location/Qualifiers 11719	Tts comparison to Arabidopsis Unpublished (2004) Contact: Chen Chen Contact: Chen Chen	Viao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., IwaH,D., Wong,G.K.S., Deng,X.W. and Wang,J. An analysis of transcriptional regulation of the rice genome and	Eukaryota; Viridiplantae; Streptopnyta; Emoryopnyta; Iracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaae; Oryza.  1 (bases 1 to 1719) Ma,L., Wangc,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M.,	CL949010. CL949010.1 GI:52361019 GSS. Oryza sativa (indica cultivar-group) Oryza sativa (indica cultivar-group)	CL949010 1719 bp DNA linear GSS 21-SEP-2004 OSIFSB002788 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.

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Percent Similarity:
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Query Match:
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                                                                        SerGlyValThrPheGlyLeuProValSerGluGlyThrAlaArgLeuLeuSerAsnSer
                                                                                                               AlaTyrPheAlaValGlyAlaProLeuLeuGlySerValGluAlaIleLysSerThrLeu
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             PheAlaSerSerLeuTrpLeuMetProPheSerLysAsnCysLysGlyAspAsnThrSer
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TTTGGTTCATCTTTATGGCTCATGCCCTTCTCAGAATATTGCAAAGCTGATAATATATAC
                                                         TCTGGAGCAACATTTGGTCTTCCAGTCAGCGAGGGAACAGCACGATTGATGTTTAATGCA
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|mol type="genomic DNA"
|/mol type="genomic DNA"
|/mol type="genomic BNA"
|/clone lib="Coryza sativa Express Library"
|/note="Oryza sativa exon trapped genomic sequence
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Solanum tuberosum (potato)
Solanum tuberosum
Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; core eudicotyledons;
Spermatophyta; Magnoliophyta; eudicotyledons;
asterids; lamiids; Solanales; Solanaceae; Solanum.

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ACCESSION VERSION KEYWORDS	RESULT 2 CK259394 LOCUS DEFINITION	Db 1	γQ	Db 1	Qy	Db 1	Ş	ეხ 1	Ş	Db 1	β	Db 1	Q.	B &	) [		Db 1	9	Db 1	γQ	ф	γO	В	VΩ	Db	γ	В	Ś	망	γQ
394.1 GI:39816372		94 AATCA	545 GlyTyr 546	34 TTTGAAGATGCTGAAAGCATTCCGGGATGGAGAACAGCCGTCTGGGAGCTTGATAAAGC	rGluSerIleProGlyLysArgThrAlaValTrpGluLeuAspLy		rAspileIleAlaAsnMetThrLysAlaProArgValLysTyrIleThrE		roGlnProGluHisAspGlySerAspValHisValGluLeuAsnValAspHi	354 TCCTACAATTCTCTCTCATGGTGCAAGAACTGGGTTGGGCCAAAAGTGAACATAACTAGG 1413	465 ProTyrHisSerLeuSerTrpCysLysAsnTrpLeuGlyProLysValAsnIleThrMet 484	294 TCCAGATCAGGTAATTCTGTTACTGGAAAGCCCAACAATTCCAGCGGAGACGGAACGGTA 1353	445 SerArgSerGlyThrValValAspGlyAsnAlaGlyProIleThrGlyAspGluThrVal 464	437 TYPELIVINES NELY SET LEU	1 PLIMI I I I GUNUUGNG I GOMANNUUNI I I VUNGOI INNU I GONI I GONI INNU I GONI I GON	7 TyrTyrPheAlaProSerGlyLysProTyrProAspAsnTrpIleIleThrAspIleIle 43	4 AGACCCCCAATAAAGAATGTGTTCTGCATAI	397 ArgProProIleLygAsnValPheCysIleTyrGlyAlaHisLeuLysThrGluValGly 416		377 HisGlnLeuLysLysLeuTyrHisAspAspProValPheAsnProLeuThrProTrpGlu 396	994 TCAGATGGTACTCTGTTTAAAACCATAAAGGATTGGGACCCTCAGAGCATAGGGCTTATC 1053	357 AlaAspGlyThrLeuPheLysAlaIleGluAspTyrAspProAspSerLysArgMetLeu 376	934 ATAACATCCAGCATGGAGTGTGGAAAGCCAACTCTATTGTCATTTTCTGCTAGGGAGGTT 993	338 MetThrSerMetGluCysGlyLeuProThrLeuLeuSerPheThrAlaArgGluLeu 356	ξ	luIleProSerThrSerValThrGluThrAla	GATGGCCCACAAACCTTGTCAC	4 Суває	766 TGGAAGCATTTCTTTGAGGGAAAGGGAGGTTGCCACCACAGACAG	PheSerGlyGlyAlaAlaLysLysAspLysArgValTy

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REFERENCE
AUTHORS
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Other EST8: EST705470 EST705471 EST705473
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr. Rockville, MD 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 946)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.
Generation of ESTs from abiotic stressed potato tissue
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Clones can be requested from the University of Arizona Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Institute via http://genome.arizona.edu/orders/
Seq primer: CAG GAA ACA GCT ATG ACC.
                                                                                                                                                                                                                SerGlyValThrPheGlyLeuProValSerGluGlyThrAlaArgLeuLeuSerAsnSer 266
                                                                                                                                                                                                                                                                                                   AlaTyrPheAlaValGlyAlaProLeuLeuGlySerValGluAlaIleLysSerThrLeu
                                                                                                                                                                                                                                                                          GCCTATTTTGCTGTTGGAGCTCCTCTTCTTGGTGCTATCGAGACAGTCAAAGCAACATTA
                    CGGAGACATTTCTCTGGTGGA---AACAGAAAATACCATCATGCCTACCATTGCGATGAG
                                                 TrpThrHisPheSerGlyGlyAlaAlaLysLysAspLysArgValTyrHisCysAspGlu 306
                                                                                                       TTTGGATCTTCTATATGGATGTTACCATTTTCAAAATATTGTACAACTGATAATGCATAT
                                                                                                                                             PheAlaSerSerLeuTrpLeuMetProPheSerLysAsnCysLysGlyAspAsnThrSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_nost="helub-tona"
/clone lib="potato abiotic stress cDNA library"
/note="Vector: pCMVSport6.1; Site 1: EcoRI; Site_2: NotI;
supplier: Solanum tuberosum var. Kennebec plants were
grown from cuttings on a 16hr light/8 hr dark cycle at 25
C for 3-4 weeks. Abiotic stress conditions were applied to
four separate sets of plants. Set 1 involved saturation of
the soil with 150 mM NaCl and tissues were harvested at
following application of the salt stress (leaves: 2hr,
6hr, 11hr, 1d, 2d, and 4d; roots:2hr, 6hr, 11hr, and 2d).
Set 2 were grown under the standard conditions and then
were water stressed by withdrawal of further watering
applications. Drought stressed plants were harvested after
cessation of watering (leaves: 3d, 5d, and 7d; roots:3d
and 5d). Set 3 were grown under the standard conditions
and then were cold stressed by placement at 4 C. Cold
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
2d. Set 4 were grown under the standard conditions and
then were harvested at 2 hr, 6 hr, 12 hr, 1 d,
2d. Set 4 were grown under the standard conditions and
then were harvested at 2 hr, 6 hr, 12 hr, 1 d,
2d and 4d and heat-stressed by placement at 35 C. Heat
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
2d and 4d and heat-stressed roots were harvested at 6 hr,
12 hr, 1 d, and 4d, RNA was isolated from all tissues and
equal RNA from each tissue and stress was pooled to
construct the cDNA library. RNA sample."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="abiotic stress treated leaf and root tissue"
lab_host="DH10B-TonA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:4113"
/clone="POAB029"
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/cultivar="Kennebec"
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70.16%
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                                                                                                                                                                                                                                                        Aquilegia formosa x Aquilegia pubescens
Aquilegia formosa x Aquilegia pubescens
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;
Ranunculaceae; Aquilegia.
                                                                                                                                                                                                                                                                                                                                                                                                                              EST1121078 Aquilegia cDNA library Aquilegia formosa x Aquilegia pubescens cDNA clone COlNX27, mRNA sequence.
Contact: Scott Hodges
Department of Ecology, Evolution and Marine
University of California, Santa Barbara
Santa Barbara, CA 93106, USA
Tel: 805 893 7813
Fax: 805 893 4724
                                                                                                                               Unpublished (2005)
Other_ESTs: EST1121077
                                                                                                                                                                     1 (bases 1 to 903)
Hodges, S.A., Rensink, W., Buell, C.R.,
Nordborg, M. and Tomkins, J.
Generation of ESTs from Aquilegia
                                                                                                                                                                                                                                                                                                                                                                                                               pubescens cDNA
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EST 02-AUG-2005

533 941

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459 658 439 419

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379 418 358

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Biology

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Seq primer: M13 Reverse.
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CAGTTATCCTTCTCTGCTAGGGAAGTGTCAGATGGAACATTATTCAGGGCTATCAAGGAA
                   LeuLeuSerPheThrAlaArgGluLeuAlaAspGlyThrLeuPheLysAlaIleGluAsp
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                                                                 ACATT - TTAGATGAAGTAGCACAACAGAATGTTTCCAGCAGGAATGTGGACTCCCTACT
                                                                                                  ThrSerValThrGluThrAlaLeuValAsnMetThrSerMetGluCysGlyLeuProThr
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/lab host="DH10B T1 (T1 and T5 phage resistance)"

/clone lib="Aquilegia cDNA library"

/clone lib="Aquilegia cDNA library"

/note="Vector: pCMV SpORT6.1; Site 1: ECORI; Site 2: NotI;

/R2, F3, and F4 lines of Aquilegia Formosa X A. pubescens
were grown from seed in greenhouses at UC Santa Barbara.
From these plants three sets of tissue were collected: 1)

Small flower buds (<10 mm) and very young inflorescences
(71 & 29% by weight respectively), 2) Medium (7-20 mm) and
large (at or near anthesis) flower buds (65 & 35% by
weight respectively) and 3) Shoot apical meristems. A
fourth set of tissue was collected from plants of A.
formosa. These plants were grown from seed in sand and at
approximately 1 month root tissue and leaf tissue of
various developmental stages were collected from each
set of tissue and pooled in the following proportions:
1.5x from sets 1 & 2, 1x from sets 3 & 4. From the pooled
total RNA, mRNA was extracted and enriched for full-length
messages and then normalized with proprietary methods by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:338618"
/clone="CO1NX27"
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80.13%
67.22%
37.84%
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Tyler,B. Not Published
Unpublished (2003)
                                                                                                                                                                                  FORWARD: BK reverse primer
BACKWARD: BK reverse primer
Platte: 029 row: F column: 13
Seq primer: BK reverse primer
High quality sequence stop: 752.
                                                                                                                                                                                                                                                                                                                                                         Contact: Tyler B
Tyler lab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phytophthora sojae
Eukaryota; stramenopiles;
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Phytophthora sojae
                                                                                                                                                                                                                                                                                                        1880 Pratt Dr., Blacksburg,
Tel: 540-231-7318
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phytophthora.
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                                                                                                                                                                                                                                                                                        Email: bmtyler@vt.edu
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                                                 /tissue_type="mycelium"
/cell_line="P6497"
                                                                                  /organism="Phytophthora
/mol_type="mRNA"
/db_xref="taxon:67593"
/clone="9HB029F13"
                                                                                                                                                                   Location/Qualifiers
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752 bp mRNA linear EST 30-OCT-200. psHB079xF13f USDA-IFAFS:Expression of Phytophthora sojae genes during infection and propagation_sHB Phytophthora sojae cDNA clone sHB029F13 5, mRNA sequence.
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/dev stage="48 hr. post infection stage"
/lab_host="Soybean plant"
/clone_lib="USDA-IFAFS:Expression of Phytophthora sojae
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Solanum tuberosum (potato)
Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                      EST
                                                                           EST705471 potato clone POAB029 5'
                                                   CK259393.1
                                                                                                   CK259393
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                                                                                                                                                                                                                                                                                                               SerIleValPheAlaHisSerMetGlyAsnAsnValPheArgTyrPheLeuGluTrpLeu 208
                                                                                                                                                                                                                                                                                                                                                                                                     GCAATAATTGCTGTTCCATATGATTGGAGATTGTCGCCCTCCAAGCTTGAAGAGCGGGAC 490
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                                                                                                                                                                                                   rPheAlaValGlyAlaProLeuLeuGlySerValGluAlaIleLy8SerThrLeuSerGl 248
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/note="Vector: pBK-CMV; Site_1: EcoR1; Site_2: Xho1"
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                                                                         abiotic stress cDNA library Solanum end, mRNA sequence.
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Other EST8: EST705470 EST705472 EST705473
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 208
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Clones can be requested from the University of Arizona
Institute via http://genome.arizona.edu/orders/.
Seq primer: ATT TAG GTG ACA CTA TAG.
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(bases 1 to 788)

Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and I
Generation of ESTs from abiotic stressed potato tissue
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rTrpThrHisPheSerGlyGlyAlaAlaLysLysAspLysArgValTyrHisCysAspGl
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/cultivar="Kennebec"
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                                                                                                                                              Plant Genomics Group
The Institute for Genomic Research
7712 Medical Center Dr, Rockville, MD 20850,
                                                                                                                                                                                                   Buell, C.R., Zheng, L., Cowles, A. and Cairney, J. Sequencing of ESTs from loblolly pine embryonic libraries Unpublished (2004)
Contact: C. Robin Buell
                                                                                                                                                                                                                                                                                                                                                                                        DR688001 832 bp mRNA linear EST 12-JUL-2005 EST1078084 Normalized pine embryo library, Lib_D Pinus taeda cDNA clone PWABZ19 3' end, mRNA sequence.
                                                                                                          Email: rbuell@tigr.org
This clone is available through TIGR. Please contact pine@tigr.org
for further information
                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; 1 (bases 1 to 832)
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DR688001.1 GI:70776477
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                                                                                          further information primer: TAA TAC GAC TCA CTA
/organism="Pinus taeda"
/mol_type="mRNA"
/cultivar="7-56 mother tree, open-pollinated tree from,
/yons, Georgia, USA"
                                                                             ocation/Qualifiers
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8.03e-99 1007.50 84.05% 70.82% 33.98%

Length:
Matches:
Conservative:
Mismatches:
Indels:

832 182 34 39

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/clone="WABZ19"
/tissue_type="Whole embryos excised from megagametophytes"
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/clone lib="Normalized pine embryo library, Lib_D"
/note="Organ: Zygotic Embryos; Vector: pGADD7-ReCAB;
Site 1: EcoRI; Site 2: ClaI; Library enriched in
transcripts present in suspension culture of Loblolly pine
(Pinus taeda L.), 7-56. Suspension culture of Loblolly pine
form ferrilized megagametophytes, according to method of
pullman et al 2003 (Pullman, G., S. Johnson, G. Peter, J.
Cairney, and N. Xu. 2003. Improving loblolly pine somatic
embryo morphology, germination, and gene expression. Plant
Cell Reports 21:74-758.) This suspension cell culture,
which contains early developing embryos and
undifferentiated embryogeneic tissue, was the source of
the RNA used for the suspension culture library.
Subtracted from this was cDNA made from a pool of RNA from
zygotic embryos and female gametophytes from all stages of
development plus somatic embryos from developmental stages
beyond susepension culture (see Clavatta VT, Morillon R,
pullman GS, Chrispeels M, Cairney J. 2001. An
aquaglyceroporin is abundantly expressed early in the
development of the suspensor and the embryo proper of
loblolly pine (pinus taeda L.). Plant physiol. 127:
1556-1567
[http://www.plantphysiol.org/cgi/content/full/127/4/1556])
RIGIN
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US-09-651.	US-09-651-651-5 (1-546) x DR688001 (1-832)
Qy	1 MetGlyAlaAsnSerLysSerValThrAlaSerPheThrValIleAlaValPhePheLeu 20
Db	61 ATGGCAGCATCATCAACTCTGTTCACAAAGATCCTTATTTTGTATACTCTTCTGGCG 120
Qy	21 IleCysGlyGlyArgThrAlaValGluAspGluThrGluPheHisGlyAspTyrSer 39
Db	121 ATCTCATTAGAGGCGCAAGAGGCCAGTGGTGAAGGGGAAACGATGGTCGGAGTACAGTTCC 180
γ	40 LysLeuSerGlyIleIleIleProGlyPheAlaSerThrGlnLeuArgAlaTrpSerIle 59
Db	181 AAGCTTTCTGGAGTTATAATTCCGGGATTTGCTTCAACGCAACTCAGAGCATGGGCCATG 240
ş	60 LeuAspCysProTyrThrProLeuAspPheAsnProLeuAspLeuValTrpLeuAspThr 79
Дb	241 CTCGATTGCCCCTTTTCTCCTCTTGATTTCCACCCGCTGGATTCTGTTTTGGCTCGACACC 300
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Дb	301 AGAAAGGTAATTTCTGTTGTGAATTGTTGGCTAAAGTGCATGATGCTTGACCCATACAAT 360
δλ	100 GlnThrAspHisProGluCysLysSerArgProAspSerGlyLeuSerAlaIleThrGlu 119
Db	361 CAAACAGACCATCCTGAATGCAGGTCGCGACCTGACACAGGTCTGTCT
β	120 LeußspProGlyTyrrleThrGlyProLeuSerThrValTrpLysGluTrpLeuLysTrp 139
Вb	421 CTCGACCCTGGTTTTATAACAGGTCCACTTTCTTCTGTTTGGAGAGAAATGGGTTCAGTGG 480
Q	140 CysValGluPheGlyIleGluAlaAsnAlaIleValAlaValProTyrAspTrpArgLeu 159
Db	481 TGTGTTGAATTTGGAGTTGAAGCAAATGCAATTTTGGCTGTTCCTTATGACTGGAGGCTA 540
Qy	160 SerProThrLysLeuGluGluArgAspLeuTyrPheHisLysLeuLysLeuThrPheGlu 179

120

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RESULT 7
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Tel: +46 90 786 5279
Fax: +46 90 786 6676
Email: bo.segerman@pl
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DN503413.1
EST.
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Sterky, F., Bhalerao, R.R., Unneberg, P., Segerman, B., Nilsson, P., Strunner, A.M., Charbonnel-Campaa, L., Lindvall, J.J., Tandre, K., Strauss, S.H., Sundberg, B., Gustafsson, P., Uhlen, M., Bhalerao, R.P. Nilsson, O., Sandberg, G., Karlsson, J., Lundeberg, J. and Jansson, S. A Populus EST resource for plant functional genomics Proc. Natl. Acad. Sci. U.S.A. 101 (38), 13951-13956 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DN503413 823 bp mRNA linear EST 10-MAR-2005
Y014D01.5pR Populus infected leaf substracted cDNA library Populus
tremula cDNA clone Y014D01 5', mRNA sequence.
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Contact: Bo Segerman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Populus tremula

Populus tremula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.
                                                                                                                                                                                                                                                                                                                                                                                                                Umea Plant Science Center,
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                                                                  (1-546)
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                                                                                                                                                                                                                                                                                                                                            bo.segerman@plantphys.
                                                                                                                                                                                                                   /clone_l
library"
                                                                                                                                                                                                                                  tissue_type="Virus/Fungal infected leaf"
/clone_lib="Populus infected leaf substracted/
                                                                                                                                                                                                                                                          /organism="Populus trem
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                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                            3.07e-94
965.50
73.94%
61.24%
32.56%
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Bhalerao, R.P.,
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cDNA clone F165
CK939714
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Sapindales; Rutaceae; Citrus.
                                        Citrus sinensis
Citrus sinensis
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                                                                                                                                                                                                                                                GluHisAspGlySerAspValHisValGluLeuAsnValAspHisGluHisGlySerAsp
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F04 Developing fruit
F1650002_IIF_F04 5',
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Citrus sinensis
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488 684 468 624 448 388

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Analysis of peel specific genes in Citrus (2004)
Unpublished (2004)
Contact: Abhaya Dandekar, PhD
CAES Genome Facility
UC Davis, Department of Pomology
One Shields Ave, Davis, CA 95616, USA
Tel: 530 752 8502
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                                   ValAsnCysTrpPheLysCysMetValLeuAspProTyrAsnGlnThrAspHisProGlu 105
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GTGAACTGTTGGCTTAAGTGCATGACACTAGATCCTTACAATCAAACAGATAATCCCGAA
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primer: WSC-F-TCCGAGATCTGGACGAGC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      california (USA). Fruit was collected on October 22, 2003, between 8 to 9 am and stored at 4C. The flavedo tissue was dissected out of developing fruit (165 DAFB) and used to isolate RNA using Trizol reagent from Invitrogen. The cDNA Library was constructed using the SMART cDNA library Kit (Clontech). The primary library was en masse evicted and plasmid DNA containing the cDNA library was isolated from the resultant bacterial population. Plasmid DNA was then transformed into ultra competent E coli cells (XLIO Gold; Stratagene). Transformants were plated out on Q-trays (2000 Cfu/tray), picked using a Qbot and archived in 384 well discharge the collection of the collectio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab host="XL10-Gold"
/lab host="XL10-Gold"
/clone lib="neveloping fruit flavedo at 165 DAFB"
/clone lib="neveloping fruit flavedo at 165 DAFB"
/note="organ: Fruit; Vector: pTriplEx2; Site_1: SfiIA;
/note="organ: Fruit; Vector: pTriplEx2; Site_1: SfiIA;
/interes: Developing citrus fruits were harvested from trees growing in the 'Citrus variety collection' in the Wolfskill experimental orchard located in Winters,
the Wolfskill experimental orchard located on October 22, 2003,
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/sex="Hermaphrodite"
/cell_type="Falvedo"
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2002)
On Jun 10, 2002 this sequence version replaced gi:21367492.
Onther ESTS: EST616039
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; saterids; lamiids; Solanales; Solanaceae; Solanum.

1 (Dases 1 to 686)

Buell, C.R., Hart, A., Baker, B., Tanksley, S., Fry, W., Smart, C., Restrepo, S., Griffiths, H., van der Hoeven, R., Tsai, J. and
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Generation of a set of potato cDNA clones for microarray analyses
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Institute. Orders can be made through URL:
                                                                                                                                                                                                                                                                                                                                                               http://genome.arizona.edu/orders/
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                                                                                                                                                                                                                                                                                                                                                                                          potato-array@tigr.org
/clone lib="Generation of a set of potato cDNA clones for microarray analyses mixed potato tissues" /note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; supplier: Combination of untreated and Phytophthora infestens-treated libraries of stolons, leaves, leaflets, axillary buds of stem explants, petioles, germinating eyes, tubers, or roots."
                                                                                                                                                                                        /organism="Solanum tuberosum"
/mol type="mRNA"
/culTivar="Kennebec or Binjte
/db xref="taxon:4113"
/clone="STMGX37"
                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                 /tissue_type="mixed tissues"
/lab_host="SOLR"
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                                                                                                                                                                                           pubescens cDNA clone DR914958
                                       Hodges,S.A., Rensink,W., Buell,C.R., Nordborg,M. and Tomkins,J.
Generation of ESTs from Aquilegia
                                                                              Aquilegia formosa x Aquilegia pubescens Aquilegia formosa x Aquilegia pubescens Eukaryota; Viridiplantae; Streptophyta; Embryo Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculaceae; Aquilegia.

1 (bases 1 to 777)
                                                                                                                                                                       DR914958.1 GI:71684321 EST.
                                                                                                                                                                                                                            DR914958
EST1106497
          Unpublished (2005)
Other_ESTs: EST1106496
Contact: Scott Hodges
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AlaHisLeuLysThrGluValGlyTyrTyrPheAlaProSerGlyLysProTyrProAsp 428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PheAsnProLeuThrProTrpGluArgProProIleLysAsnValPheCysIleTyrGly 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGTCCTTTTCTGCTCGTGAAGTCTCTGACGGAACCTTTTTCAAAGCCATAAAGAATTAT 120
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                                                                                                                                                                                                                                                                                                      GAAAGTTTTCCAGGAACGAGAACAGCAGTTTGGGAGCTTGATAAAGCAAATCAC 654
                                                                                                                                                                                                                                                                                                                   GluSerIleProGlyLysArgThrAlaValTrpGluLeuAspLysSerGlyTyr 546
                                                                                                                                                                                                                                                                                                                                                            GluHisAspGlySerAspValHisValGluLeuAsnValAspHisGluHisGlySerAsp 508
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                                                                                                                                                                                                              777 bp mRNA linear cDNA library Aquilegia formosa CO1LG72, mRNA sequence.
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             437
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Department of Ecology, Evolution and Marine Biology University of California, Santa Barbara Santa Barbara, CA 93106, USA Tel: 805 893 7813 Fax: 805 893 4724
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                         flower buds, leaves and roots"

/lab host="DH10B T1 (T1 and T5 phage resistance)"

/clome lib="Aquilegia cDNA library"

/clome lib="Aquilegia cDNA library"

/note="vector: pCMV SPORT6.1; Site 1: EcoRI; Site 2: NotI;

F2, F3, and F4 lines of Aquilegia Formosa X A. pubescens
were grown from seed in greenhouses at UC Santa Barbara.
From these plants three sets of tissue were collected: 1)

Small flower buds (<10 mm) and very young inflorescences

(71 & 29% by weight respectively), 2) Medium (7-20 mm) and

large (at or near anthesis) flower buds (65 & 35% by
weight respectively) and 3) Shoot apical meristems. A

fourth set of tissue was collected from plants of A.

formosa. These plants were grown from seed in sand and at
approximately 1 month root tissue and leaf tissue of
various developmental stages were collected (84 % 16% by
weight respectively). Total RNA was extracted from each
set of tissue and pooled in the following proportions:
1.5X from sets 1 & 2, 1X from sets 3 & 4. From the pooled
total RNA, mRNA was extracted and enriched for full-length
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**ROOTE TO THE PLANT TO THE PROOTE TO THE POOLED T
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messages and then normalized with proprietary methods Invitrogen."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tissue type="mixed shoot and floral apical meristems, lower buds, leaves and roots"
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/clone="CO1LG72"
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mol_type="mRNA"
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456	TyrGluThrGluGlySerLeuValSerArgSerGlyThrValValAspGlyAsnAlaGly 456	euValSerArgSerGly	luThrGluGlySerLe	TyrGl	437	S
361	AACTGGATCATAACTGATATTGTT	CAAACCATATCCTGAT	ACTITGCTCCGAGTGC	TATTA	302	40
436	TyrTyrPheAlaProSerGlyLysProTyrProAspAsnTrpIleIleThrAspIleIle	\yLysProTyrProAsp	/rPheAlaProSerGl		417	Ş
301	ATAGATTCAAAGACTGAGGTTGGG	PATTTTGCATATATGGA	CACCTTTGAAGAACAT	AGACC	242	밁
416	ArgProProIleLysAsnValPheCysIleTyrGlyAlaHisLeuLysThrGluValGly 416	lPheCysIleTyrGly	coProIleLysAsnVa		397	ρ
241	TTAAATCCTCTTACACCATGGGAT	TCATGATGATGCAGTG	VACTAGAGAAGTTATA		182	ф
396	HisGlnLeuLysLysLeuTyrHisAspAspProValPheAsnProLeuThrProTrpGlu	rHisAspAspProVal	  hLeuLysLysLeuTy	HisGl	377	γo
181	GATCCAGATACAGAAAAACTATTG	GGCTATCAAGGAATAT	TGGAACATTATTCAG		122	멍
376	AlaAspGlyThrLeuPheLysAlaIleGluAspTyrAspProAspSerLysArgMetLeu	sAlaIleGluAspTyr	pGlyThrLeuPheLy		357	Ş
121	TTATCCTTCTCTGCTAGGGAAGTG	TGGACTCCCTACTCAG	TTCCAGCAGGGAATG	AATGI	62	<del>d</del> d
356	AsnMetThrSerMetGluCysGlyLeuProThrLeuLeuSerPheThrAlaArgGluLeu	/sGlyLeuProThrLeu	etThrSerMetGluCy		337	Ş
61	TCAATTACAGAAGTAGCACAACAG	CATTGATGCTTATCCA	TCCTTCAACTCGAGG	GAAAT	N	뫄
336	GluIleProSerThrSerValThrGluThrAlaLeuVal 336	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	GluIleProSerThr		324	Ş
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CK260764
CK260764.1 GI:39817742
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/.
Seq primer: ATT TAG GTG ACA CTA TAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr. Rockville, MD 20850, USA
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Other_ESTs: EST706843
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/table | Particle | Pa
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lab_host="DH10B-TonA"
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/clone="POAB552"
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BG600021
BG600021.1 GI:13617157
                                                                                                                                                                          BG600021 792 bp
EST504916 cSTS Solanum tuberosum
                 Solanum tuberosum
                                       Solanum tuberosum
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2d. Set 4 were grown under the standard conditions and then were heat stressed by placement at 35 C. Heat stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 12d and 4d and heat-stressed roots were harvested at 6 h 12 hr, 1 d, and 4d. RNA was isolated from all tissues a equal RNA from each tissue and stress was pooled to construct the cDNA library. RNA sample." hr,

i. No.:  re: cent Similarity:     Local Similarity cy Match:	arity: nilarity:	1.02e-88 916.00 84.19% 74.42% 30.89%	Length: Matches: Conservative: Mismatches: Indels: Gaps:	968 1160 21 34 0	
)9-651-651	-5 (1-546)	x CK260764 (1-9	168)		
329 19	SerValThr	GluThrAlaLeuValA           saaaCTGCCCAAACCA	\8nMetThrSerMetG    :::::  ACTTGTCTGGAATGG	SerValThrGluThrAlaLeuValAsnMetThrSerMetGluCY9GlyLeuProThrLeu 3	348 78
349 79	LeuSerPhe'	ThrAlaArgGluLeuA :::          rcrgcrcgrgaagrci	\laAspGlyThrLeuP 		368 138
369 139	AspProAsp	SerLysArgMetLeuH    :::   ::: AGTGAAAGACTCTTTC	iisGlnLeuLysLysL              ACCTTTTAAAAAAGT	AspProAspSerLysArgMetLeuHisGlnLeuLysLysLeuTyrHisAspAspProVal 3	961
389 199	PheAsnPro	LeuThrProTrpGlu [‡] 	ArgProProIleLy8A            AGACCACCTCTCAAGA	PheAsnProLeuThrProTrpGluArgProProIleLyBAsnValPheCysIleTyrGly 4	408 258
409 259	AlaHisLeu GTAGATTCG	LysthrGluValGly7               hagaCTGAGGTTGGT7	[yrTyrPheAlaPros 	AlaHisLeuLysThrGluValGlyTyrTyrPheAlaProSerGlyLysProTyrProAsp 4	428 318
429 319	AsnTrpIle	IleThrAspIleIle7           aTAACAGATGTGATA7	TyrGluThrGluGlyS         argaaarcgaaggar	ASHTYPI1eIleThrASpI1eIleTyrGluThrGluGlySerLeuValSerArgSerGly 4	448 378
449 379	ThrValVal :::    AATCTGGTT	AspGlyAsnAlaGlyF :::       GAAGGAAACCCTGGTC	ProlleThrGlyAspG :::       3CAACAAGTGGGGATG	ThrValValAspGlyAsnAlaGlyProlleThrGlyAspGluThrValProTyrHisSer 4 :::   :::	468 438
469 439	LeuSerTrp          CTCTCCTGG	CysLysAsnTrpLeu(              GCAAGAATTGGCTGC	GlyProLysValAsn1 	LeuSerTrpCysLysAsmTrpLeuGlyProLysValAsmIleThrMetAlaProGlnPro 4	498
489 499	GluHisAsp          GAGCATGAT	GlySerAspValHis\        GGCTCAGCTGTACAA(	ValGluLeuAsnVal <i>I</i>      TGCATCAAAATATAC	GluhisaspGlySerAspValHisValGluLeuAsnValAspHisGluHisGlySerAsp 5	508
509 559	IleIleAla        ATCATTCCC	AsnMetThrLysAlai            AATATGACAAAGTTAO	ProArgValLysTyr1 	IleIleAlaAsnMetThrLysAlaProArgValLysTyrIleThrPheTyrGluAspSer	528 618
529 619	GluSerIle        GAAAGTTTT	GluSerileProGlyLyBArgThrAlavalTrpGluLeuAspLy8        	AlavalTrpGluLeuf                  CAGTTTGGGAGCTTC	\spLys 543        ATAAA 663	
ULT 12					

(potato)

cDNA clone

linear EST 07-MAR-2003 e cSTS27C13 5' sequence,

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Percent Similarity:
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Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamiids; Solanales; Solanaceae; Solanum.

1 (bases 1 to 792)
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This clone can be obtained fi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Institute. Orders can be made through URL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SerValThrGluThrAlaLeuValAsnMetThrSerMetGluCysGlyLeuProThrLeu 348
AATCTGGTTGAAGGAAACCCTGGTGCAACAAGTGGGGATGAGACGGTGCCATACCATTCC
                          ThrValValAspGlyAsnAlaGlyProIleThrGlyAspGluThrValProTyrHisSer 468
                                                                                                                                                        GTAGATTCGAAGACTGAGGTTGGTTACTATTTTGCACCAAGTGGGAAGCCTTATCCTGAT 300
                                                                                                                                                                              AlaHisLeuLysThrGluValGlyTyrTyrPheAlaProSerGlyLysProTyrProAsp 428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCAGTTGTAGAAACTGCCCAAACCAACTTGTCTGGAATGGAATGTGGATTCCCGGCCACA 60
                                                                                             AsnTrpIleIleThrAspIleIleTyrGluThrGluGlySerLeuValSerArgSerGly 448
                                                                         AATTGGATTATAACAGATGTGATATATGAAATCGAAGGATCTCTGTATTCCCGGTCAGGA
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/note-"Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
/note-"Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; Various sizes of sprouting eyes (2mm to 15mm) were
taken from tubers. The tubers were incubated at 26C in the
dark for 2-3 weeks prior to sprouting. The eyes were
frozen in liquid nitrogen immediately upon removal from
tubers."
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/cultivar="Kennebec"
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cLEC71F15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Generation of ESTs from tomato callus tissue Unpublished (1999)
Contact: CUGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alcala, J., Vrebalov, J., White, R., Matern, A.L., Vision, T., Holt, I.E., Liang, F., Upton, J., Craven, M.B., Bowman, C.L., Roming, C.M., Fraser, C.M., Martin, G.B., Tankeley, S.D. and
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                           IleAlaValPhePheLeuIleCysGlyGlyArgThrAlaValGluAspGluThrGluPhe 34
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/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
Xhol, supplier: Glovannoni laboratory; cLEC - Cotyledons
of seedlings 7-10 days post-germination were excised, cut
at both ends and placed on MS medium with no selection.
Mixed callus was harvested at 25 and 40 days and included
undifferentiated masses. Tomato Callus EST Library"
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5' end, mRNA sequenc
                                                                                                                                                                                                                                                                                                                                                                /dev_stage="25-40 days old"
/lab_host="XL1-Blue MRF'"
                                                                                                                                                                                                                                                                                                                                                                                            tissue_type="callus"
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/clone="cLEC71F15"
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/cultivar="TA496"
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Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Akiyama,K., Enju,A., Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y. and Shinozaki,K. Large scale analysis of Arabidopsis full-length cDNA Unpublished (2002)
                                                                                   Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 596)
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AU237072.1 GI:19876241
EST.
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Plant Functional Genomics Research Group
RIKEN Genomic Science Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074,
Tel: 81-298-36-4359
Fax: 81-298-36-9060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length coNA library was constructed essentially
an Arabidopsis full-length coNA library was constructed essentially
as reported previously (Seki et al., 1998).cNNA cleaved with BamHI
and XhoI was ligated to modified Lambda FLC-1 vector (Carrinci et
al., submitted for publication) digested with BamHI and SalI. This
clone is in a modified psluescript vector. Please visit our web
site (http://www.gsc.riken.go.jp/e/plant/index _e.html) for further
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                                                                                         GTTGAGTTTGGTNTAGAAGCAAATGCAATTGTCGCTGTTCCATACGATTGGAGATNGTCA
                                                                                                          ValGluPheGlyIleGluAlaAsnAlaIleValAlaValProTyrAspTrpArgLeuSer
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/lab_host="DH10B"
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/note="Site_1: BamHI;
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tomato callus Lycopersicon aculentum CDNA clone  1 G:16218653  con esculentum (Solanum lycopersicum) con esculentum (Solanum lycopersicum) con esculentum (Solanum lycopersicum) con esculentum (Solanum lycopersicum) con esculentum (Solanales; Solanaceae; Solanum; Lycopersicum) lycopersicum location, Solanales; Solanaceae; Solanum; Lycopersicum location (Solanales; Solanaceae; Solanum; Lycopersicum) location (Solanaceae; Solanum; Lycopersicum) location (Solanum; Lycopersicum) location (S	8	Qy Db	<b>Qy</b> рь 1	Qy Db 1	Ob Db	US-09-651-6	Alignment S Pred. No.: Score: Sercent Sim Best Local Query Match DB:	ORIGIN	FEATURES Bource		TITLE JOURNAL COMMENT	REFERENCE AUTHORS	LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM
77 9 9 4 6d ced ced ced ced ced ced ced ced ced ce	5 LeuAspProTyrAsnGlnThrAspHisProGluCysLysSerArgProAspSerGlyLeu	5 ValTrpLeuAspThrThrLysLeuLeuSerAlaValAsnCy 	55 ArgAlaTrpSerIleLeuAspCysProTyrThrProLeuAspPheAsnProLeuAspLeu	35 HisGlyAspTyrSerLysLeuSerGlyIleIleIleProGlyPheAlaSerThrGlnLeu 54	IleAlaValPhePheLeuIleCysGlyGlyArgThrAlaValGluAspGluThrGluPhe :::	651-	Scores:       7.17e-81       Length:       63         :       841.50       Matches:       16         !milarity:       72.24%       Conservative:       12         ! Similarity:       67.35%       Mismatches:       17         :       28.38%       Indels:       52         :       3       Gaps:       2	B1"  days old" e MRF'" callus" cestlus' cestribt SK(-); Site_1: EcoRI; Site_ wescribt SK(-); Site_1: EcoRI; Site_ mic Research; cLEC - Cotyledons of mic Research; cLEC - Cotyledons of s post-germination were excised, cut ed on MS medium with no selection. M ed at 25 and 40 days and included dasses. Tomato Callus EST Library"	Institute Seq primer: T3. Seq primer: T3. Location/Qualifiers e	Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Email: http://www.genome.clemson.edu/orders/index.html This clone is available through the Clemson University Genomic	Martin (B. Tanksley, S.D. and Giovannoni, J. Generation of ESTs from tomato callus tissue (2001) Unpublished (2001) Contact: CUGI	eudicotyledons; core solanaceae; Solanum; ,R., Vision,T., Karan	B1922233  EST542136 tomato callus Lycopersicon esculentum cC CLEC76P18 5' end, mRNA sequence. B1922233 B1922233.1 GI:16218653 BST. Lycopersicon esculentum (Solanum lycopersicum) Lycopersicon esculentum

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Copyright (c) 1993 - 2005 Compugen Ltd.
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181 GACTGTCCATACACTCCGGTTGGACTTCAATCCGCTCGACCTCGTATGGCTAGGACACCACT 240	121 CTATCGGGTATAATCATTCCGGGATTTGCGTCGACGCAGCAGCGAGCG	121 CTATCGGGTATAATCATTCCGGGATTTGCGTCGACGCAGCTACGAGCGTGGTCGATCCTT 180	61 ATTTGCGGTGGCCGAACTGCGGTGGAGGATGAGACCGAGTTTCACGGCGACTACTCGAAG 120	61 ATTTGCGGTGGCCGAACTGCGGTGGAGGATGAGACCGAGTTTCACGGCGACTACTCGAAG 120	1 ATGGGAGCGAATTCGAAATCAGTAACGGCTTCCTTCACCGTCATCGCCGTTTTTTTCTTG 60	1 ATGGGAGCGAAATCGGTAACGGCTTCCTTCACCGTCATCGCCGTTTTTTTT	/ Match 100.0%; Score 1641; DB 6; Length 1641; Local Similarity 100.0%; Pred. No. 0; ndels 0; Gaps 0; local; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	/organism="Arabidopsis thaliana" /mol_type="unassigned DNA" /db_xref="taxon:3702"	11641	Location/Qualifiers	٠,	Patent. WO 0116308-2 4 08-MAR-2001.	Lassner, M. and van Eenennaam, A.		kukaryota; viridipiantae; streptopnyta; kmoryopnyta; iracneopnyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids: eurosids II; Brassicales: Brassicaceae; Arabidoosis.	Arabidopsis thaliana	Arabidopsis thaliana (thale cress)	MA090311.1 G1:13444180	CT . 13444187	Sequence 4 from Patent W00116308.	1641 kg DNA 1:5004 DAT

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/OUZANISHE "MEDICAGO ETHICATULA"  /OOL TYPE="MRNA"  /OD Xref="taxon:3880"  /Clone lib="Samuel Roberts Noble Foundation Medicago /Cote="fabaceae; sequence derived from EST clones BE321377  and BI267156"  82 . 1980  /DOTE="enzyme involved in the metabolism of phospholipids and sterols" /codon start=1 /product="lecithine cholesterol acyltransferase-like protein" /protein" /protein id="AAN77002.1" /db_xref="GI:25992001" /fanslation="MANKPFLIFSILLAFLAVAGGDSGGGSELDYSKLSGIIIPGFAS /TLRAMSILDCFYSFLDENPLDLYMLDTTKLLSAVNCMLKCMLLDPYNQTDHPDCKSR PDSGLSGITELDPGYITGPLSSVWKEWIKWCIEFGIEANAIIAVPYDWRLSPSMLEER DLYFHKLKLTFETAFKLRGGPSLVFGHSLGNNVFRYFLEWLKLEIAPKHYIQWLDQHI	Molecular France	1 (bases 1 to 2609) NOITIEL,A., Benveniste,P., Banas,A., Stymne,S. and Bouvier-Nave,P. Expression in yeast of a novel phospholipase A1 cDNA from Arabidopsis thaliana Eur. J. Biochem. 271 (18), 3752-3764 (2004) 1535352 2 (bases 1 to 2609) Benveniste,P., Bouvier-Nave,P., Schaller,H. and Noiriel,A.	AF493159 AF493159 Medicago truncatula lecithine cholesterol acyltransferase-like protein mrNA, complete cds. AF493159 AF493159 AF493159.1 GI:25992000 Medicago truncatula (barrel medic)	.621 CTTGATAAAAGTGGGTATTAA 1641 	.561 TACATAACCTTTTATGAAGACTCTGAGAGCATTCCGGGGAAGAGAACCGCAGTCTGGGAG 1620 	01 GTTGATCATGAGCATGGGTCAGACATCATAGCTAACATGACAAAAGCACCAAGGGTTAAG 1560 	21 GATTGAGACGGTACCCTAATCAATTGACTGGTTGGATGGA	21

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ANLSGMECGLPTQLSFSARELADSGFFKAIEDVDDSKRLLYQLEKSYLDEDFULNUT
PMDRPPIKNVFCIYGSNSKTKVGYYFAPSGKPYPDNWIITDVVYEYEGSLVTRSGNLV
EGNPGSISGDETVPYNSLSWCKNWLGFKVNITTAPQSEEDGSDVQIIDLNVEHHYGDDI
VPNMTRFPRIKXITYYEDSESLPGKRTAVWELDKANHRUN VRSSVLMRELMLENWRDI
UPDAKSEFYTKAKRGPLRDEDCYWDYGKARCAWPEYCEYRYVFGDVHLGQSCRLRYTS
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                                                                                                                                                       JOURNAL
Dahlqvist,A., Stahl,U., Lenman,M., Banas,A., Ronne,H. and Stymne,S.
Novel class enzyme in biosynthesis pathway of triacrylglycerol
production and recombinant DNA molecule encoding the enzyme
L Patent: JP 2002541783-A 8 10-DEC-2002;
BASF PLANT SCIENCE GMBH
OS Arabidopsis thaliana (thale cress)
PN JP 2002541783-A/8
PN JP 2002541783-A/8
PD 10-DEC-2002
PP 10-DEC-2002
PP 28-MAR-2000 JP 2000609586
PR 01-APR-1999 EP 99106656.4,10-JUN-1999 EP 99111321.8 PR
07-FEB-2000 US 60/180687
PI ANDERS DAHLOVIST,ULF STAHL,MARIT LENMAN,ANTONI BANAS PI
,HANS RONNE,STEN STYMNE
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1 (bases 1 to 3896)
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JP 2002541783-A/8.
Arabidopsis thaliana (thale
Arabidopsis thaliana
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3896 bp DNA linear PAT 17-JUL-2003
Novel class enzyme in biosynthesis pathway of triacrylglycerol
production and recombinant DNA molecule encoding the enzyme.
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ACCESSION
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BD271633
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (Dases 1 to 3996)

Dahlqvist,A., Stahl,U., Lenman,M., Banas,A., Ronne,H. and Stymne,S novel class enzyme in biosynthesis pathway of triacrylglycerol production and recombinant DNA molecule encoding the enzyme Patent: JP 2002541783-A 18 10-DEC-2002; BASF PLANT SCIENCE GMBH
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                                                                                                                                                BD271633.1 GI:33081401

TP 2002541783-A/18.

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana
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3896 bp DNA linear PAT 17-JUL-2003 Novel class enzyme in biosynthesis pathway of triacrylglycerol production and recombinant DNA molecule encoding the enzyme.
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PN JP 200254783-A/18

PD 10-DEC-2002

PF 28-MAR-2000 JP 2000609586

PF 01-APR-1999 EP 99106656.4,10-JUN-1999 EP 99111321.8 PR
07-FEB-2000 US 60/180687

PI ANDERS DAHLQVIST,ULF STAHL,MARIT LENMAN,ANTONI BANAS PI
,HANS RONNE,STEN STYNNE
PC C12N15/09,A01H5/00,C12N1/19,C12N5/10,C12N9/10,C12P7/64// PC
(C12P7/64,C12R1:645),(C12P7/64,G12R1:91),C12N15/00,C12N5/00 CC
(C12P7/64,C12R1:645),DTONORDE IN DIOSYNTHESIS PATHWAY

OF triacrylglycerol

CC and recombinant DNA molecule encoding the enzyme FH Key

CC and recombinant DNA molecule encoding the enzyme FH Key
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Arabidopsis thallana (thale cress)
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/mol_type="genomic DNA"
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Banas, A., Stahl, U., Stymne, S., Lenman, M., Ronne, H. and Dahlqvist, A new class of enzymes in the biosynthetic pathway for the production of triacylglycerol and recombinant dna molecules encoding these enzymes
Patent: WO 0060095-A 30 12-OCT-2000;
BASF PLANT SCIENCE GMBH (DE); BANAS ANTONI (PL); STAHL ULF (SE)
                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Patent: WO 0060095-A II 12-OCT-2000;
BASF PLANT SCIENCE GWBH (DE); BANAS
STYMME STEN (SE); LENMAN MARIT (SE)
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                                                                                                                              Arabidopsis thaliana
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/mol_type="unassigned DNA"
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2 (bases 1 to 119914)

Pederspiel, N.A., Palm, C.J., Conway, A.B., Kurtz, D.B., Conway, A.R., Au, M., Araujo, R., Buehler, E., Dewar, K., Feng, J., Kim, C., Li, Y., Oji, O., Osborne, B.I., Shinn, P., Sun, H., Toriumi, M., Vyotskaia, V., Yu, G., Ecker, J., Theologis, A. and Davis, R.W.
                                                                                                                                                                      1 (bases 1 to 119914)
Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Araujo, R., Huizar, L., Rowley, D., Buehler, E., Dunn, P., Altafi, H., Araujo, R., Huizar, L., Kim, C., Lenz, C., Li, J., Liu, S., Gonzalez, A., Kremenetskaia, I., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vysotskaia, V.S., Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W.
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Arabidopsis thaliana
                     Yu,G., Ecker,J., Direct Submission
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/db_xref="taxon:3702"
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Pred. No. 2.8e-67;
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Biochemistry, Stanford University/DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLN 30-OCT-2002
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REFERENCE
AUTHORS
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JOURNAL
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genes with similarity to proteins in the databases are described as 'putative', '-like' or 'similar to'. Genes that have BST similarity but no significant protein similarity are described as 'unknown proteins'. Genes that are amoutated only on gene prediction software are described as 'hypothetical proteins'. The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, http://compbio.ornl.gov/section/index.html), GENSCAN (Chris Burge, http://gnomic.stanford.edu/~chris/GENSCANW.html), Pexa (V.Solovyev & A.Salamov, Sanger Centre, http://genomic.stanger.ac.uk/), and NetPlantGene (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, http://www.cbs.dtu.dk/NetPlantGene.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pederspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Araujo, R., Huizar, L., Rowley, D., Buehler, E., Dunn, P. Gonzalez, A., Kremenetskaia, I., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vyotskaia, V., Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Direct Submission
Submitted (30-DEC-1998) DNA Sequencing and Technology Center,
Submitted University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     On Dec 30, 1998 this sequence version replaced gi:2734094. Bases 1-9262 of clone F2LM11 overlap with bases 68998-78259 of 'TAMU' BAC clone F2DD22 (AC002411) and bases 119525-119914 of clone F21M11 overlap with bases 1-389 of 'TAMU' BAC clone F21B7 (AC002560).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (30-JAW-1999) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Altafi, H., Araujo, R., Huizar, L., Rowley, D., Buehler, E., Dunn, P. Gonzalez, A., Kremenetskaia, I., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vyotskaia, V., Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  e-mail for correspondence: arab@sequence.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 119914)
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LSSFSDEQSCSTSCIEDCLASEMSCNCAIGVDNGFAYTLDGLLKEEFLEARISEARDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F21M11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10501. .10551,10685. .10781,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic_DN:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="F21M11.1"
join(7684. .7866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="overlap with"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone="F21M11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'chromosome="I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7684. .7866,7965. .8027,8122. .8160,8250. .8381
.8728,8875. .9893,10003. .10256,10344. .10410,
....10551,10685. .10781,10885. .10913)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC002411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in this region are annotated in the F21M11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bases 68998-78259 of 'IGF'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dunn, P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
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GDFYKGYKEDLQNLYKVAGGTILNTEDELGAESSNNVNDRSSSIVYNVIDPPHGCAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(join(16835. .17185,17274. .17392,17491. .1765
17795. .17885,17982. .18079,18175. .18361,18504. .18604,
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22102. .22178,22542. .22758,22920. .23064,23343. .23442,
23599. .23693,24021. .24072,24227. .24298,24441. .24647)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (16835. .20238)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SKGRTKOKOSOKENSNETADOBEKRDSSSFCTDPOLIDLITLSVEKKCR EFKKLRNOE
LAVDASLSTWLSTSESGSECNSASMYTLTPEKLKKSTSCYSKFLRINHDDRFVLCALTL
EDIKOPSATSTPRKSPSKSPDETFILGTVGGYWGNRSKAIDCGSASSFKGIPNTSSKY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MLDQISGNHTHEKLSVETAEPHHLNDRVHIVEEIPKASVIPITE
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DSLHNPTKEVYTQDIGDKTEEIDSKLRRSNETVRDGNHYDGQGVLNPVENLTQWKSAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(join(14567. .14641,14787. .15831,15906.
16327. .16362))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(join(14004..14312,14565..14641,14787. 15906..16006,16327..16362))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MDRTWFLSLTIASLLVGVVSAGDWNILNQLRGLGSSSSONGIVS
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KHFGSMCCSKSKCDGMDAMIFDIDDTLLSTIFYHKNKGFFGGEKLNGTTRFEDMIOKK
APAVPHMKKLYHDIRERGIKIFLISSRKEYLRSATVDNLIQAGYYGMSNLMLRGLEDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="F21M11.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (14004. .16362)
/gene="F21M11.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QKEVKQYKSEKRKWLMSLGYRVWGVMGDQWSSFAGCPLPRRTFKLPNSIYYVA"
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/gene="F21M11.2"
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WGSEERLEGDKALCLDGMFYGNISRPLNHRCLDANLIEIPVQVETPDQHYYHLAFFTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'gene="F21M11.4"
'note="Hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="F21M11.4"
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/db_xref="GI:4204286"
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/db_xref="GI:4204285"
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/gene="F21M11.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene="F21M11.3"
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and 110C2XP, g
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/gene="F21M11.5" /note="Hypothetical protein"

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/gene="F21M11.7"
complement (join (29264. .31015,31312.
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kLvpppvnpiskksstaaaepigsnqlmlagylsheyltqgtlfgeqmnqaraqaess
kIkpshtvepaeecepkrkryrevanllrsdgaqlpgivnpaqlarflkl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="F21M11.6"
/note="Unknown protein; Location of EST8
gb|H76794 and 203124XP, gb|AA605510"
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28007. .28465
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27777. .28734
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DGTLFKAIEDYDPDSKRMLHQLKKYVPFFVIRNIAHRSSLAGFLLYHDDPVFNPLTPW
ERPPIKNVFCIYGAHLKTEVGYYFAPSGKPYPDDWIITDIIYETEGSLVSRSGTVVDG
NAGPITGDETVPYHSLSKEVKNWLGPKUNITMAPQILIGKIKQQPEHDGSDYHVELNVD
HEHGSDIIANMTKAPRVKYITFYEDSESIPGKRTAVWELDKSGY*
27777. . 28734
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11pgfastqlraws1ldcpytfldfnrldlwldtrkllsavncmfkcwvldpyngotd
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KWLDQHIHAYFAVGAPLLGSVEAIKSTLSGVTFGLFVSEGTARLLSNSFASSLFILMFF
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/protein_id="AAD10670.1"
/db_xref="GI:4204289"
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/db_xref="GI:4204287"
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Pred. No. 3.1
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Direct Submission
Submitted (07-MAY-2003) Shusei Sato, Kazusa DNA Research Institute, Submitted (07-MAY-2003) Shusei Sato, Kazusa DNA Research Institute, Department of Plant Gene Research; 2-6-7 Kazusa-kamatari, Kisarazu, Chiba 292-0818, Japan (E-mail:ssato@kazusa.or.jp, Chiba 292-0818, Japan (E-mail:ssato@kazusa.or.jp, URL:http://www.kazusa.or.jp/, Tel:81-438-52-3935 (ex.2337),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93398 bp DNA linear PLN 2:
Lotus corniculatus var. japonicus genomic DNA, chromosome
Clone:LjT06108, TM0082b, complete sequence.
AP006356
                                                                                                                                                                      Asamizu,E., Kato,T., Sato,S., Nakamura,Y., Kaneko,T. and Tabata,S. Structural Analysis of a Lotus japonicus Genome. IV. Sequence Features and Mapping of seventy-three TAC clones which cover the 7.5 Mb Regions of the Genome DNA Res. (2003) In press DNA Res. (2003) In press (bases 1 to 93398)
                                                                                                                                                                                                                                                                                                                                                                                     Lotus corniculatus var. japonicus (Lotus japonicus)
Lotus corniculatus var. japonicus
Lotus corniculatus var. japonicus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
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Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Zea.
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/mol_type="unassigned
/db_xref="taxon:4577"
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Pred. No. 1.6e-39;
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Best Local Similarity
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(E-mail:tasaskienias.affrc.go.jp./ ORL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)
On Jun 1, 2004 this sequence version replaced gi:34740243.
Genes were predicted from the integrated results of the following:
GENSCAN (http://CCR-081.mit.edu/GENSCAN.html), FGENESH
(http://www.softberry.com//, GeneMark/), GlimmerM
(http://www.softberry.com//, GeneMark/), GlimmerM
(http://rgp.dna.affrc.go.jp/RiceHMM/), SplicePredictor
(http://rgp.dna.affrc.go.jp/RiceHMM/), SplicePredictor
(http://rgp.dna.affrc.go.jp/RiceHMM/), SplicePredictor
(http://rgp.dna.affrc.go.jp/RiceHMM/), SplicePredictor
(http://rgp.dna.affrc.go.jp/RiceHMM/), SplicePredictor
(http://rgp.dna.affrc.go.jp/RiceHMM/), BLASTN and BLASTX. The
genomic sequence was searched against NCBI NonRedundant Protein
database, nr (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA
sequence database at RGP or DDBJ Protein homologies of the coding
regions were searched against NCBI NonRedundant Protein database
with BLASTP. ESTs represent the identified cDNA sequences using
BLASTN with the corresponding DDBJ accession no. and RGP clone ID.
Full-length cDNAs represent the identified cDNA sequences using
BLASTN with the corresponding DDBJ accession no.
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Submitted (29-AUG-2001) Takuji Sasaki, National Institute of Syrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sasaki,T., Matsumoto,T. and Yamamoto,
Oryza sativa nipponbare(GA3) genomic
clone:OJ1293_E04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 2, BAC clone:OJ1293_E04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sasaki, T., Matsumoto, T. and Yamamoto, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Published Only in Database (2001)
2 (bases 1 to 118192)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chromosome="6"
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/variety="japonicus"
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Pred. No. 1.7e-22;
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The orientation of the sequence is from -21Ml3 to Ml3rev of the BAC clone. This sequence of OJ1293_EO4 clone has an overlap with OSJNBa0053L11 (DDBU: AP005691) clone at 5' end and with P0643F09 (DDBU: AP005111) at 3' end. The sequence was generated by combining Monsanto and RGP-Japan sequencing data. Detailed information on overlap and assembly quality together with annotation of this entry is available at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://rgp.dna.affrc.go.jp/GenomeSeq.html.
                                                                                           ADSDAVWASFLPRNLPDLADGELSPAPASKKELFLRLSDGPYLLSDRLMSMWLDRETG
AKCYMLSARSLVIIWGDTPHYWRWIPLTDSRPAEGAELIDVCWLBIRGRIHSKWLSPN
STYAAYMVPKIADEFYGLDAPFQEASVSLGGRGSTKIVCVQSYDSEDEEVPENYWPMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8501. .8573,8672. .9312)
/gene="OJ1293_E04.2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MELRQNCVQKLGDSKVPWKFVPDFPFSEVVEFLKGYRVEVCGKI
PCKMLSGNSNYAAYIVFVVAEDSCGLASVWVAIVGVGGRQSTRQVCLDSSNRNDYYYE
GEIEVPQDGSVJLPQERADGWMELELGEFYNQEGNNQGEVCFSLVKPKAGRWLSNGGL
VIQGIEIRPKIS"
                              IGPLLRRRARRRDRRLVLDEGVTVPQKRTDEWMELEMGEFINEEGEDGEVCFSLMETK
GGNWKRGLIVQGIEIRLKKSG"
                                                                                                                                                                                                                                                                                                                                                           contains full-length cDNA(s):
phloem-specific lectin"
                                                                                                                                                                                           /produCt="F-box family protein-like"
/protein id="BAD21652.1"
/db xref="G1:47847859"
/translation="MEEEGEGLCEIARLPEELLSAAISRASPRDACHAAAVSPAFRAA
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join(11875. 12242,12368. 12486,13292. ...

/gene="OJ1293_E04.3"

/note="supported by full-length cDNA(8):

join(11953. 12242,12368. 12486,13292. ...

/gene="OJ1293_E04.3"
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|oin(6482..6988,7071.
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|join(<1863. .1936,2024. .>2468)
|gene="0J1293_E04.1"
|note="gtart and end point are not identified"
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(mol_type="genomic DNA"
(cultivar="Nipponbare"
                                                                                                                                                                                                                                                                                                                                                                                                                           note="contains EST(s): AU092429(C50563)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="supporced by full-length cDNA(s):
|oin(11964. .12242,12368. .12486,13292. .
|gene="OJ1293_E04.3"
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/protein_id="BAD21651.1"
/db_xref="GI:47847858"
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/gene="0J1293_E04.1"
/note="predicted by GeneMark.hmm
                                                                                                                                                                                                                                                                                                                               codon_start=1
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chromosome="2"
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.15901,16106. .16272,16375.
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   .16439,16593.
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/protein_id="BAD21655.1"
/db_xref="G1:47847862"
/db_xref="G1:47847862"
/translation="MDLPLVTLLLLAHAAAMVAMQAAARRRATCYLLDYACHKPSD
/translation="MDLPLVTLLLLAHAAAMVAMQAAARRRATCYLLDYACHKPSD
DRKVTTELAGAIIERNKRLGLEBYRFLLKVIVNSGIGEHTYSPRNVLDAREDCFTLRD
ALDEMDDFFDDAVAAVLARAAVSPRDVDLLVINVGSFSPSPSLADRVVKRFFGLRDDVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(27410. .29382)
/gene="0J1293 E04.5"
complement(join(<27410. .27558,29301. .>29382))
/gene="0J1293 E04.5"
/note="start and end point are not identified"
complement(join(27410. .27558,29301. .29382))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WKGMGAHVDLFYRKELFLRGFDDEMRTVVÅSNLEGRGIRLHPGTNLSELSKTADGIKV
VTDKGEBIIADVVLFATGRT BNSQRLMLEAAGVEVDNIGAIKVDDYSRTSVPNIMAVG
DVTNRINLTFYALMBATGESKTVFGGOPTKPDYRDVPGAVFSIPPLSVGGLESCOALE
EAKSDVLVYTSSFNPMKNSISKROEKTVMKLVVDSETDKVLGASMCGPDAPEIIOGMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="markmlkdeevevavtdggsydydlfv1gagsggvrgsrtsasf
garvalgepehjis5mwqgghggtcvlrgcvpkkilvvgssfrggepdaknegmein
gdinenwkrllenktoglivrlngvydridgsgcvymlegagslvdahtyveytkepgsk
Qrytakhillatgspaqrvnipgkelaitsdealsleelpkravilgggyiavefasi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probably inactive due to including stop codon(s) in CDS" join(16132 ...16272,16375 ...16439,16593 ...16662,16996 ...17165 ...17368,18290 ...18363,18462 ...18545,19079 ...19166, 19260 ...19341,19675 ...19748,19971 ...20078,20180 ...20244, 20814 ...2027,21141 ...21240,21337 ...21390,21469 ...21364),/genee_MOJ1293_E04.4-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="OJ1293_E04.4-1"

join(15841. .15901,16106. .16272,16375. .16439,16593. .16662,

join(15941. .15901,16106. .18363,18462. .18545,

16966. .17067,17165. .17368,18290. .18363,18462. .18545,

19079. .19166,19260. .19341,19675. .19748,19971. .20078,

19079. .20244,20814. .20927,21141. .21240,21337. .21390,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="contains EST(s): D22281(C10676),AU102120(C10676)
contains full-length cDNA(s): AK100446,AK058270"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21469. .21825)
/gene="OJ1293_E04.4-1"
/note="supported by full
15858. .20860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VALKCGATKATFDSTVGIHPSAAEEFVTMRTLTRRVSPSSKPKTNL'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="glutathione reductase"
/protein_id="BAD21653.1"
/db_xref="GI:47847860"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16996. .17067,17165. .17368,18290. .18363,18462. .18545, 19079. .19166,19260. .19341,19675. .19748,19971. .20078, 20180. .20244,20814. .20927,21141. .21240,21337. .21390,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          non-coding transcript
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="OJ1293_E04.4-2"
/note="contains full-length cDNA(s): AK066398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15858.
                                                                                                                                                                                           product="putative fatty acid elongase 3-ketoacyl-CoA
                                                                                                                                                                                                                                                       /gene="OJ1293_E04.6"
/note="contains full-length cDNA(s): AK107210"
                                                                                                                                                                                                                                                                                                                              /note="supporTed by full-length cDNA(8): AK107210"
31845. .33236
                                                                                                                                                                                                                                                                                                                                                                                          gene="0J1293_804.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAENRTTPTGNSSSHRGRLLHRRPRLSRQTD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 translation="MELRSHRIYWPLYMLEMKWRGVRVRMRALSTCGTPTPAASAGQS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="hypothetical protein"
/protein_id="BAD21654.1"
/db_xref="GI:47847861"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="OJ1293_E04.5"
/note="predicted by GENSCAN etc."
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15858. .20860
                                                                                                                                                                                                                                codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .17067,
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JOURNAL REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:Esasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:B1-298-38-7441, Fax:B1-298-38-7468)

Tel:B1-298-38-7441, Fax:B1-298-38-7468)

On Jun 1, 2004 this sequence version replaced gi:38564216. Genes were predicted from the integrated results of the following: GENSCAN (http://CCR-081.mit.edu/GENSCAN.html), FGENESH (http://www.softberry.com/), GeneMark.hmm (http://www.softberry.com/), GeneMark.hmm (http://www.tigr.org/tdb/glimmerm/glmr_form.html), RiceHMM (http://www.tigr.org/tdb/glimmerm/glmr_form.html), RiceHMM (http://sp.dna.affrc.go.jp/RiceHMM/), SplicePredictor (http://splicePredictor (http
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147123 bp DNA line
Oryza sativa (japonica cultivar-group) genomic
BAC clone:OSJNBa0053L11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Published Only in Database (2002)
2 (bases 1 to 147123)
Sasaki.T., Matsumoto,T. and Katayose,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sasaki,T., Matsumoto,T. and Katayose,Y. Oryza sativa nipponbare(GA3) genomic DN clone:OSJNBa0053L11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridilplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (05-SEP-2002) Takuji Sasaki, National Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCTCCCAAGCATTACATCCGATGGCTTGACGAACATATACATGCATACTTTGCAGTTGG 64375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCTCATTCCATGGGTAATAATGTGTTTCGCTACTTTCTGGAATGGTTGAAACTAGAAATC 64434
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35504. .35704
/gene="OJ1293_E04.7"
/note="hypothetical ORF
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LPKAAVAAFTENLQRLAPRILDAGELAFFAARLLLRKLLRKAAGAAAKINFKTGVD
HFCLHPGGTAVIEAVRKSLGLDSYDVEPARWALHRWGNTSASSLWYVLSYMEAKRKL
AGDRVLMVTFGSGFKCNSSYWVVTKDLADAGAWEDCIHDYPPANLVNPYMEKFGWVND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-' and '-like protein'. A gene without significant homology to any protein but with full-length cDNA or EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted by two or more gene prediction programs is classified as a 'hypothetical' protein according to IRGSP standard. A gene predicted by a single gene prediction program is also classified as a probable 'hypothetical' protein and is included as a miscellaneous feature of the sequence.

The orientation of the sequence is from -21M13 to M13rev of the BAC clone. This sequence of OSJNBA005311 clone has an overlap with P0016F11 (DDBJ: AP004120) at 3' end. Detailed information on overlap and assembly quality together with annotation of this entry is available at http://rm.dna.affrc.orienGenerger.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               available
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              join(4436...4894,4982...5164,5251...5600,6156...6617)
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SANAEGLRPLWLSASALSHGSVTSAITRNSYAVNVATSRGSPSLPPRATPPAARGYVA
SPPRRDTANPSTRHGGQTAAATRWPPLGSTCG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Join(210. .282,431. .528,603. .662)

/gene="OSJNBA0053L1.1"

Join(210. .282,431. .528,603. .662)

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/note="hypothetical ORP
       complement(join(<7826. .8214,8309. .>8435))
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                                                                                                                                                   PVTSKCEDEGNQMVKPYKFSNQRLRDLGLEFTPLRKSLHEAIECLQRKGHLPVVTVAQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    this category is not included in IRGSP standard"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             predicted by GENSCAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                join(2264. .2293,2852. .3226)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="OSJNBa0053L11"
join(210. .282,431. .5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         db_xref="taxon:39947"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cultivar="Nipponbare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      at http://rgp.dna.affrc.go.jp/GenomeSeq.html.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .147123
                                                                                .8435)
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                                                                                                                                                                                                                                                                                       gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                               AHLRCRRLVFFLTRLTYYAAISGHLRFHRRPPSSPPTGVFTVIDGRLCSHIGHFCHHO
GEYYKKKONGSVRTSPPARLDRRRLVFFPARLAFMFPLLGVYVFTDRLAFAADWCFRL
HGWPLCRRCWASTSSPTGRELVRRRLVLPPARLAYYAAVGRLRLHRPAASAADWCFR
LHGWFIMPFLLGVYVFTDRLAFAADWCFRLHGWPIMPFLLGVYVFTDRPFRPPTGA
SACTAGLLCRRCWASTSSPTGLPSPPTGVSACTAGLYATVVGRRLRLHRLACLGRRCRL
VFPPARLAFWFPLLGVYTDRLAFAADAWCFRLHGWFLCRRCWASTSSPTGLPSPPT
TGVSACTAGLLCRRCWASTSSPTGRLVRRRLVLPPARLAYYAAVVGRIRLHRPACLER
TGVSACTAGLLCRRCWASTSSPTGRLVRRRLVLPPARLAYYAAVVGRIRLHRPACLER
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predicted by GENSCAN
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FCRQKDVSLLHMYCYAKTYMAEWAATAEAAKRGLELAVVVPSWTMGPMLQRALMLSSTH
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                                                                                                              /note="start and end point are not identified"
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RRILVPPTRVAYYAAAVGRLELHRRPAFAAADWCFRLHGWPTBUPDLLGYVDFTAGLS
PSPPSGASAYTAGLLCRRCWASTTSSPPAYLRRRRVVPPPTRLAYYAAAVGRLRLHRRP
ASVAAEWCLRLHGWPTMPPLLGVYDFTAGLPPSPPSGASAYTAGLLCRRCWMSTSSLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="OSJNBa0053L11.4"
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                                                                                                                                                                         complement(join(<18994. .19134,19786. .>19818))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MAAAGPSSSAPPRPGAGVATMVAGRRGDSAAGGRGALHGRRGAAAVVADVVETKLATTAADCGSCRDAGPRHCSGCERRARDAFLHDASDPRVALHLRSASPRPDLDVWRLVALASDGGGWTGVAVAVAVAVAMAMVADGGGCGSDGGGYRRCYLWRRWLKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         this category is not included in IRGSP standard" 
15304. .18533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (join (12759.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9814. .11214
                                                                                                                                                                                                                                                      /gene="OSJNBa0053L11.8"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         join(<9814. .10128,10328. .10525,10605. .10954,11058. .>11214)
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/potic="start and end point are not identified"
/poin(9814. .10128,10328. .10525,10605. .10954,11058. .11214)
/gene="OSJNB80053L11.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IRLTVRHRRR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene="OSJNBa0053L11.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               oin(<15304. .16325,17024. .>18533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="similar to Oryza sativa chromosome 1, P0497A05.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .12851,13439.
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RESULT 12
AP004882/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 138;
                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126651 AACTGCAGGTTAACTTTTGAAACTGCATTGAAACTTCGAGGAGGGCCTTCTTTAGTGTTT
                                                                                                                                               Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (B-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)

NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as goon as it is available and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sasaki,T., Matsumoto,T. and Yamamoto,K. Oryza sativa nipponbare(GA3) genomic DN clone:P0511E12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HTG; HTGS PHASE2.

Oryza satīva (japonica cultivar-group)

Oryza satīva (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa (japonica cultivar-group)
*** SEQUENCING IN PROGRESS ***
APPO4883
                                                                                                                                                                                                                                                                                                                                                                                              Submitted (20-MAR-2002) Takuji Sasaki, National Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Published Only in Database (2002)
2 (bases 1 to 158971)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AP004882
                                                                                                                                                                                                                                                                                                                                                                                                                   Sasaki,T., Matsumoto,T. and Yamamoto,K. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AP004882.1 GI:19698302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ehrhartoideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCTCCCAAGCATTACATCCGATGGCTTGACGAACATATACATGCATACTTTGCAGTTGG 126473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCACCAAAACATTATTTGAAGTGGCTTGATCAGCATATCCATGCTTATTTCGCTGTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCTCATTCCATGGGTAATAATGTGTTTCGCTACTTTCTGGAATGGTTGAAACTAGAAATC 126532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCCCATTCAATGGGTAATAATGTCTTCAGATACTTTCTGGAATGGCTGAGGCTAGAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGCTCAAGTTGACCTTTGAAACTGCTTTAAAACTCCGTGGCGGCCCTTCTATAGTATTT
                                                                                                                by the finished sequence as soon as it is the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (join(21959. .22112,22149. /gene="OSJNBA0053111.9" /note="hypothetical ORF predicted by GlimmerM this category is not included in IRGS
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complement/--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KDVVVGEVVKLAK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="hypothetical protein"
/protein_id="BAD22382.1"
/db_xref="GI:47848530"
  /cultivar="Nipponbare"
/db_xref="taxon:39947"
                                     organism="Oryza sativa
mol_type="genomic DNA"
                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      translation="MEVKKPVGNSQICVEGVQVEILNIGESLVVVKYHGIACRDVEVH/
                                                                            .158971
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 113.4; DB 8;
Pred. No. 3.7e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            is not included in IRGSP standard"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                          (japonica cultivar-group)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chromosome
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Best Local (
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REFERENCE AUTHORS

KEYWORDS VERSION ACCESSION

REFERENCE

JOURNAL TITLE

AUTHORS TITLE

JOURNAL

COMMENT

FEATURES

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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel class enzyme in biosynthesis pathway
of triacrylglycerol
CC production
CC and recombinant DNA molecule encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dahlqvist,A., Stahl,U., Lenman,M., Banas,A., Ronne,H. and Stymne,S. Novel Class enzyme in biosynthesis pathway of triacrylglycerol production and recombinant DNA molecule encoding the enzyme Patent: JP 2002541783-A 9 10-DEC-2002,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon. 1 (bases 1 to 709)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel class enzyme in biosynthesis pathway of triacrylglycerol production and recombinant DNA molecule encoding the enzyme. BD271624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ,HANS RONNE,STEN STYMNE
PC C12N15/09,A01H5/00,C12N1/19,C12N5/10,C12N9/10,C12P7/64// PC (C12P7/64,C12R1:645),(C12P7/64,C12R1:91),C12N15/00,C12N5/00 CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASF PLANT SCIENCE GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lycopersicon esculentum 
Lycopersicon esculentum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JP 2002541783-A/9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BD271624.1 GI:33081392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-FEB-2000 US 60/180687
PI ANDERS DAHLQVIST,ULF STAHL,MARIT LENMAN,ANTONI BANAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
CATGTGGAACTAAATGTTGATCATGAGCATGGGTCAGACATCATAGCTAACATGACAAAA 1545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCACCAAAACATTATTTGAAGTGGCTTGATCAGCATATCCATGCTTATTTCGCTGTTGG 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCCCATTCAATGGGTAATAATGTCTTCAGATACTTTCTGGAATGGCTGAGGCTAGAAATT 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAGCTCAAGTTGACCTTTGAAACTGCTTTAAAACTCCGTGGCGGCCCTTCTATAGTATTT
                                                                    CTGGGGCCAAAAGTGAACATAACAAGGACACCACAGTCAGAGCATGAT-GTTCAGATGTA
                                                                                                          GCTCCCAAGCATTACATCCGATGGCTTGACGAACATATACATGCATACTTTGCAGTTGG 58060
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                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-MAR-2000 JP 2000609586
01-APR-1999 EP 99106656
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                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                              /organism="Lycopersicon
/mol_type="genomic DNA"
/db_xref="taxon:4081"
                                                                                                                                                                                                                                                                                                                                             /organism='Lycopersicon
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="P0511E12"
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                                                                                                                                                     Score 110.4; DB 6
Pred. No. 2.3e-20;
0; Mismatches 51
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Pred. No. 3.7e-21;
0; Mismatches 41
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                                                                                                                                                                                                                                                                                                                        Matches 152;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dahlqvist,A., Stahl,U., Lenman,M., Banas,A., Ronne,H. and Stymne,S.
Novel class enzyme in biosynthesis pathway of triacrylglycerol
production and recombinant DNA molecule encoding the enzyme
AL Patent: JP 2002541783-A 19 10-DEC-2002;
BASF PLANT SCIENCE GMBH

OS Lycopersicon esculentum (tomato)
PN JP 2002541783-A/19
PD 10-DEC-2002
PF 28-MAR-2000 JP 2006609586
PR 01-APR-1999 EP 99106656.4,10-JUN-1999 EP 99111321.8 PR
07-PEB-2000 US 60/180687
O7-PEB-2000 US 60/180687
PI ANDERS DAHLQVIST, ULF STAHL, MARIT LENMAN, ANTONI BANAS PI
,HANS RONNE, STEN STYMNE
PC C12N15/09,A01H5/00,C12N1/19,C12N5/10,C12N9/10,C12P7/64// PC
(C12P7/64,C12R1:645),(C12P7/64,C12R1:91),C12N15/00,C12N5/00 CC
Novel class enzyme in biosynthesis pathway
of triacrylglycerol
CC production
CC and recombinant DNA molecule encoding the enzyme FH Key
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Lycopersicon esculentum
Lycopersicon esculentum
Eycopersicon esculentum
Eycopersicon
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
Lycopersicon.
Lycopersicon.
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BD271634
BD271634.1 GI:33081402
JP 2002541783-A/19.
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                                                                                                                                                                                                                                                                   GCACCAAGGGTTAAGTACATAACCTTTTATGAAGACTCTGAGAGCATTCCGGGGAAGAGA 1605
                       ACCGCAGTCTGGGAGCTTGATAAA 1629
                                                                            TTACCTACAATGAAGTACATAACCTATTATGAGGATTCTGAAAGTTTTCCAGGGACAAGA
                                                                                                      GCACCAAGGGTTAAGTACATAACCTTTTATGAAGACTCTGAGAGCATTCCGGGGAAGAGA 1605
                                                                                                                                                             CAAGTGCATCTAAATATAGAGCATCAACATGGTGAAGATATCATTCCCAATATGACAAAG
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asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
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CC The present sequence encodes for Arabidopsis thaliana
CC lecithin:cholesterol acyltransferase=like 2 (LCAT2). Several novel
CC polynuclectides encoding the plant sterol acyltransferases LCAT
CC (AASO01081-AAS01104, AAS01341) and ACAT (acyl COA:cholesterol
CC eacyltransferase-like; AAS01341) and ACAT (acyl COA:cholesterol
CC related open reading frame, LRO1 gene sequence (AAS01342), and a rat ACAT
CC (AAS01105) cDNA sequence are also described. The polynuclectides encoding
CC LCAT or ACAT are used to produce LCAT or ACAT polypeptides. They can also
be used in a recombinant construct to transform a host cell (preferably
CC derease the sterol content of the host cell or plant. It can be used to
CC alter oil production of the cell or plant, preferably by increasing it.
CC The oil of the plant or the plant itself is used as a food product, or as
CC untritional or distary supplements, or in pharmaceutical compositions for
CC lowering cholesterol. The oil can be used in foods e.g. margarine,
CC cheese, processed meat, pasta, sauces, cereals, desserts, dipp, chips,
CC baked goods, pastries, cookies, snack bars, confections, chocolates, and
CC beverages. The alteration in sterol content and/or composition can also
CC provide a plant with tolerance to stress and insect damage
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CC acyltransferase polypeptide can produce fatty acid esters and/or fatty CC acid thioesters such as triacylglycerols, diacylglycerols, monoacylglycerols, phospholipids, glycolipids, lysolipids, waxesters, CC acylated carbohydrates and acylated amino acids. Also described: (1) a nucleotide sequence molecule (II) comprising at least one promoter region CC which functions in a host, where the promoter region is operably linked to at least one (I), which is operably linked to at least one non-CC translated region which functions in a host; (2) a vector comprising (II) CC; (3) a host cell comprising (II) or the vector; (4) producing an CC improved active membrane independent acyltransferase polypeptide, (2) a vector comprising (II) CC comprising providing the above host cell and a growth medium preparing a host cell culture, culturing the host cell and a growth medium preparing a host cell culture and recovering the improved active membrane independent acyltransferase polypeptide; (5) a polypeptide obtained by the method in CC independent acyltransferase polypeptide; (6) an oligonucleotide comprising the above polypeptide; (6) an oligonucleotide comprising the above polypeptide at least is an improved active membrane independent conditions; and (7) a kit comprising the above polypeptide and a stabiliser. The nucleic acid CC molecule (I) and the polypeptide are useful in producing structured CC lipids or fat-soluble molecules, in removing undestrable fat or in CC modifying lipids present in animal and plant raw material. The present xx
                                        Query Match
Best Local Simi
Matches 1625;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acyltransferase; enzyme; membrane-spanning region; acid ester; active membrane independent acyltransferase; fatty acid ester; fatty acid thioester; triacylglycerol; diacylglycerol; monoacylglycerol; phospholipid; glycolipid; lysolipid; waxester; acylated carbohydrate; acylated amino acid; structured lipid; fat-soluble molecule; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a nucleotide sequence (I) derived from nucleotide sequence encoding an acyltransferase polypeptide comprising least one membrane-spanning region. (I) encodes an improved active membrane independent acyltransferase polypeptide in which at least one amino acid residue of the membrane-spanning region has been deleted and/or substituted as compared to the original acyltransferase polypeptide, where the encoded active membrane independent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleotide sequence encoding an improved acyltransferase polypeptide, useful for producing structured lipids or fat-soluble molecules, in removing undesirable fat or in modifying lipids in animal or plant raw
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29-MAY-2002; 2002US-0383889P.
20-JAN-2003; 2003SE-00000142.
                                                                                                                                 Sequence 1902 BP;
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                GAAGACTATGACCCAGATAGCAAGAGGGATGTTACACCCAGTTAAAGAAGT
                                                       CCCACCCTTTTGTCTTTCACAGCCCGTGAACTAGCAGATGGGACTCTTTTCAAAGCAATA
                                                                                                              GTGTATCCATCAGTTACAGAAACAGCTCTAGTCAACATGACCAGCATGGAATGTGGCCTT
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GAAGACTATGACCCAGATAGCAAGAGGATGTTACACCAGTTAAAGAAGT
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                                                                                                                                         GTTACAGAAACAGCTCTAGTCAACATGACCAGCATGGAATGTGGCCTT 1035
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Pred. No. 1.8e-74;
0; Mismatches 2
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AAC64448 standard; DNA; 3896 ₽₽

12-FEB-2001 (first entry)

Arabidopsis thaliana PDAT genomic DNA SEQ IJ NO:10b

RESULT 4
AAC644A68
ID AAC66
XX AAC66
XX AAC6
XX AAC6
XX AAC6
XX AAC6
XX PD 12-F
XX FAB
XX FBAT
XX FBAT PDAT; phospholipid:diacylglycerol acyltransferase; triacylglycerol; EST; expressed sequence tag; fatty acid; oil content; ds.

Arabidopsis thaliana

WO200060095-A2

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10-JUN-1999;
07-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phospholipid:diacylglycerol acyltransferase enzymes in the biosynthetic pathway for triacylglycerol production and DNAs encoding them, useful for producing triacylglycerol, or for transforming any cell or organism to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oil content
                        GAAGACTATGACCCAGATAGCAAGAGGATGTTACACCAGTTAAAGAAGT 1144
                                                                         CCCACCCTTTTGTCTTTCACAGCCCGTGAACTAGCAGATGGGACTCTTTTCAAAGCAATA 1095
                                                                                                                 ------GTTACAGAAACAGCTCTAGTCAACATGACCAGCATGGAATGTGGCCTT
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                                                                                                                                                                                                                                                                                                                                        TTCAAAGAATTGCAAGGGTGATAACACATCCTGGACGCATTTTTCTGGGGGTGCTGCAAA
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2000US-0180687P.
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Pred. No. 1.8
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RESULT 5 AAS01096

TTGGATCCAGGTTACATAACAGGTCCTCTTTCTACTGTCTGGAAAGAGTGGCTTAAGTGG

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                                                                                                                                                                                                                                                                  The present sequence for corn LCAT (lecithin:cholesterol acyltransferase-CC like) EST sequence #3 is closely related to the Arabidopsis thaliana CC LCATZ sequence. Several novel polynucleotides encoding the plant sterol CC cayltransferases LCAT (AASO01081-AASO1104, AASO1341) and ACAT (acyl CC cA; cholesterol acyltransferase-like; AASO1311-AASO1341) are described. A CC yeast LCAT (Easterol acyltransferase-like; AASO1311-AASO1319) are described. A CC polynucleotides encoding LCAT or ACAT are used to produce LCAT or ACAT (CC polypeptides. They can also be used in a recombinant construct to polypeptides. They can also be used in a recombinant construct to construct is used to increase or decrease the sterol content of the host CC cell or plant. It can be used to alter oil production of the cell or CC plant, preferably by increasing it. The oil of the plant or the plant CC itself is used as a food product, or as nutritional or dietary CC supplements, or in pharmaceutical compositions for lowering cholesterol. The oil can be used in foods e.g. margarine, butter, cooking oil, and dressings. confections, chocolates, and beverages. The CC cookies, snack bars, confections, chocolates, and beverages. The alteration in sterol content and/or composition can also provide a plant content and/or composition can also provide a plant can be trace to stress and insert damage.
                                                                                                                                              Query Match
Best Local S
Matches 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid encoding plant lecithin:cholesterol acyltransferase acyltransferase-like or acyl (coenzyme A) CoA:cholesterol acyltransferase -like polypeptides, for modifying the sterol content and oil production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lecithin: cholesterol acyltransferase-like; LCAT; sterol acyltransfer acyl CoA: cholesterol acyltransferase-like; ACAT; plant oil; cooking nutritional supplement; dairy product; food product; salad dressing; corn; Arabidopsis thaliana; expressed sequence tag; EST; ss.
                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 5; Page
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                                                                                                                                                                                                                                                           tolerance to stress and
                                      298
                                                                                                              238
   95
                                                                                                                                                  222;
                                                                                                                                                                 Similarity
                            CAAACAGACCATCCCGAGTGTAAGTCACGGCCTGACAGTGGTCTTTCAGCCATCACAGAA 357
                                                                                                ACTAAGCTTCTTTCTGCTGTTCAACTGCTGGTTTAAGTGTATGGTGCTAGATCCTTATAAT
                                                                                                                                                                                                                      328 BP; 86 A; 68
                                                                          CAGATAGACCATCCCGAATGCAAGTCAAGGCCTGATAGTGGTC-TTCTGCAATTACAGAG
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                                                                                                                                              Score 176.2; 1
Pred. No. 9.2e
0; Mismatches
                                                                                                                                                                                                                      73 G; 101 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                           insect damage
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nes 58;
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oil; cooking oil;
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RESULT 6
AAC64449
ID AAC6
XX AC6
XX AC6
XX PDAT
CYCO
XX PDAT
KW EST;
XX LYCO
XX LYCO
PN WO20
XX LYCO
PN 12-O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phospholipid:diacylglycerol acyltransferase enzymes in the bio pathway for triacylglycerol production and DNAs encoding them, producing triacylglycerol, or for transforming any cell or org
                                                                                                                                                                                                                                                                    Sequence
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10-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC64449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAC64449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                increase oil content.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BADI ) BASF
     1486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000-665012/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           phospholipid:diacylglycerol acyltransferase; triacylglycerol;
expressed sequence tag; fatty acid; oil content; ss.
                                                                                                                                                                                      Similarity
                                                                                                709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCACCAACCAAATTGGAAGAGCGTGACCTTTACTTTCACAA 518
  CATGTGGAACTAAATGTTGATCATGAGCATGGGTCAGACATCATAGCTAACATGACAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCCCCATCAATGCTTGAGGAGAGAGATCTGTACTTTCACAA 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGTGTAGAGTTTGGCATTGAAGCTAATGCAATTATCGCTGTTTCCGTATGATTGGAGACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGTGTTGAGTTTGGTATAGAAGCAAATGCAATTGTCGCTGTTCCATACGATTGGAGATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGGACCCTGGTTATATAACAGGTCCTCTCTCTTCAGTATGGAAAGAATGGGTCAAATGG
                                                    CTGGGGCCAMAAGTGAACATAACAAGGACACCACAGTCAGAGCATGAT
                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                 BP; 226 A; 121 C; 161 G; 201 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000WO-EP002701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99EP-00106656.
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                                                                                                                                                                                 6.78;
74.58;
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                                                                                                                                                             0
                                                                                                                                                           Score 110.4; DB 3;
Pred. No. 1.1e-23;
0; Mismatches 51;
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                                                                                                                                                                                                          Length 709;
                                                                                                                                                             Indels
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                                                    -GTTCAGATGTA
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nem, useful for
                                                                                                                                                           1.
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1486

CATGTGGAACTAAATGTTGATCATGAGCATGGGTCAGACATCATAGCTAACATGACAAAA 1545

CTGGGGCCAAAAGTGAACATAACAAGGACACCACAGTCAGAGCATGAT-GTTCAGATGTA

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ARESULT 7
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  Query Match
Best Local Similarity
Matches 152; Conserv
                                                                                                                                                                                                    The present invention describes an enzyme for catalysing (in an acyl-CoA-independent reaction) the transfer of fatty acids from phospholipids to diacylglycerol in the biosynthetic pathway for the production of triacylglycerol (TAG). The enzyme is designated as phospholipid:diacylglycerol acyltransferase (PDAT). The enzyme and the nucleotides encoding them are useful for producing TAG and/or TAG with uncommon fatty acids. The enzyme and the nucleotide are also useful for transforming any cell or organism in order to be expressed in this cell or organism and result in an altered, preferably increased oil content of this cell or organism. The present sequence represents the Lycopersicon
                                                                                                                            Sequence
                                                                                                                                                                                   esculentum PDAT nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 6; Page 62; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Phospholipid:diacylglycerol acyltransferase enapathway for triacylglycerol production and DNAs pathway for triacylglycerol, or for transforming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dahlqvist A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-APR-1999;
10-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-665012/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PDAT; phospholipid:diacylglycerol acyltransferase; triacylglycerol; TAG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BADI ) BASF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               oil content.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCACCAAGGGTTAAGTACATAACCTTTTATGAAGACTCTGAGAGCATTCCGGGGAAGAGA 1605
                                                                                                                               709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCGCAGTCTGGGAGCTTGATAAA 1629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTACCTACAATGAAGTACATAACCTATTATGAGGATTCTGAAAGTTTTTCCAGGGACAAGA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACAGCAGTTTGGGAGCTTGATAAA
                                                                                                                               BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99EP-00106656.
99EP-00111321.
2000US-0180687P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence
                                                                                                                            226 A; 120 C; 162 G; 201
                                        6.7%;
74.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA; 709
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lenman M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cag;
              Score 110.4;
Pred. No. 1.1e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Banas A,
.4; DB 3;
.1.1e-23;
... 51;
                                                                                                                               T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e enzymes in the biosynthetic DNAs encoding them, useful for ming any cell or organism to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ronne
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                                                                                                                               U; 0 Other;
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                                                                           709;
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RESULT 8
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                                  The present sequence for corn LCAT (lecithin:cholesterol acyltransferase-CC like) EST sequence #4 is closely related to the Arabidopsis thaliana CC LCATZ sequence. Several novel polynucleotides encoding the plant sterol CC cayltransferases LCAT (AASO01081-AASO1104, AASO1341) and ACAT (acyl CC cA:cholesterol acyltransferase-like; AASO1311-AASO1319) are described. A CC yeast LCAT related open reading frame, LRO1 gene sequence (AASO1342), and CC arat ACAT (AASO1105) cDNA sequence are also described. The CC polynucleotides encoding LCAT or ACAT are used to produce LCAT or ACAT construct is used to increase or ACAT are used to produce LCAT or ACAT construct is used to increase or decrease the sterol content of the host CC coll or plant. It can be used to alter oil production of the cell or CC cell or plant. It can be used to alter oil production of the cell or CC plant, preferably by increasing it. The oil of the plant or the plant cc itself is used as a food product, or as nutritional or dietary construct is used as a food product, or as nutritional or dietary coll can be used in foods e.g. margarine, butter, cooking oil, and CC dressings e.g. salad dressings, mayonnaise, cheese, processed meat, CC pasta, sauces, cereals, desserts, dips, baked goods, pastries, CC cooktes, snack bars, confections, chocolates, and beverages. The CC alteration in sterol content and/or composition can also provide a plant or content and or content and or composition can also provide a plant or content and or composition can also provide a plant or content and or composition can also provide a plant or content and or composition can also provide a plant or content and or composition can also provide a plant or content and or composition can also provide a plant or content and or composition can also provide a plant or content and or composition can also provide a plant or content and or composition can also provide a plant or content and or composition can also provide a plant or content and or composition can also provide a plant or co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid encoding plant lecithin:cholesterol acyltransferase acyltransferase-like or acyl (coenzyme A) CoA:cholesterol acyltransferase-like polypeptides, for modifying the sterol content and oil production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lassner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-AUG-2000; 2000WO-US023863.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Corn sterol acyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAS01097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MONS ) MONSANTO CO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; cDNA; 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCGCAGTCTGGGAGCTTGATAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90; 127pp; English
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 150;
The present invention describes a nucleotide sequence (I) derived from nucleotide sequence encoding an acyltransferase polypeptide comprising least one membrane-spanning region. (I) encodes an improved active membrane independent acyltransferase polypeptide in which at least one amino acid residue of the membrane-spanning region has been deleted and/or substituted as compared to the original acyltransferase polypeptide, where the encoded active membrane independent acyltransferase polypeptide can produce fatty acid esters and/or fatty acid thioesters such as triacylglycerols, diacylglycerols,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fatty acid thioester; triacylglycerol; diacylglycerol; monoacylglycerol; phospholipid; glycolipid; lysolipid; waxester; acylated carbohydrate; acylated amino acid; structured lipid; fat-soluble molecule; gene; ds.
                                                                                                                                                                                   New nucleotide sequence encoding an improved acyltransferase polypeptide, useful for producing structured lipids or fat-soluble molecules, in removing undesirable fat or in modifying lipids in animal or plant raw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acyltransferase; enzyme; membrane-spanning reactive membrane independent acyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schizosaccharomyces pombe acyltransferase DNA sequence
                                                                                                                                             Claim 5;
                                                                                                                                                                                                                                                                                    Dahlqvist A,
                                                                                                                                                                                                                                                                                                                                                                       29-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                                                                    28-MAY-2003;
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                                                                                                                                                                                                                                                                                                                 (SCAN-) SCANBI SCANDINAVIAN BIOTECHNOLOGY RES
                                                                                                                                                                                                                                             2004-053268/05
DB; ADF47832.
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                                                                                                                                              SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTGTCTGGAAAGAGTGGCTTAAGTGGTGTTGAGTTTGGTATAGAAGCAAATGCAATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTTCACAAATTAAAGTT 197
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; 2002US-0383889P.
; 2003SE-00000142.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry
                                                                                                                                                                                                                                                                                     Ghosal
                                                                                                                                             NO 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA; 1872
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                                                                                                                                           91pp; English
                                                                                                                                                                                                                                                                                     Lindqvist Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 109; DB 5
Pred. No. 2e-23;
D; Mismatches
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                                                                                                                                                                                                                                                                                       Banas
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RESULT 10
ADF47817
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                        acyltransferase; enzyme; membrane-spanning region; active membrane independent acyltransferase; fatty acid ester; fatty acid ester; triacylglycerol, diacylglycerol; monoacylglycerol; phospholipid; glycolipid; lysolipid; waxester; acylated carbohydrate; acylated amino acid; structured lipid; fat-soluble molecule; yeast; gene
Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                     Yeast membrane independent acyltransferase DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                            26-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADF47817 standard; DNA; 1701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGTTAATGATCATATTGAAGCATTTATAAATATATCGGGATCTTTGATTGGAGCACCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTTGATCAGCATATCCATGCTTATTTCGCTGTTGGAGCTCCTCTTCTTGGTTCTGTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TACGTACTATTTTTTAAGTGGGTTGAAGCTGAGGGCTACGGAAATGGTGGACCGACTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTTCAGATACTTTCTGGAATGGCTGAGGCTAGAAATTGCACCAAAACATTATTTGAAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAGCAACATTGTACATAAGAAAAAGGTAGTGTTGATTTCTCACTCCATGGGTTCACAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGCTTTAAAACTCCGTGGCGGCCCTTCTATAGTATTTTGCCCATTCAATGGGTAATAATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATATGCAAATTTAGAGGAACGTGATAAATATTTTTCAAAGTTAAAAATGTTCATTGAGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCAACCAAATTGGAAGAGCGTGACCTTTACTTTCACAAGCTCAAGTTGACCTTTGAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGCTGCAATTGGTTATGAGCCTAATAACATGTTAAGTGCTTCTTACGATTGGCGGTTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGTTGAGTTTGGTATAGAAGCAAATGCAATTGTCGCTGTTCCATACGATTGGAGATTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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Pred. No. 4.1e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       174;
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                                                                                                    gene;
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548

AACTCCGTGGCGGCCCTTCTATAGTATTTGCCCATTCAATGGGTAATAATGTCTTCAGAT ATCTAGAAAGACGCGATAGGTACTTTACGAAGCTAAAGGAACAAATCGAACTGTTTCATC AATTGGAAGAGCGTGACCTTTACTTTCACAAGCTCAAGTTGACCTTTGAAACTGCTTTAA

649 547

710 809

ACTTTATGAAATGGGTCGAGGCTGAAGGCCCTCTTTACGGTAATGGTGGTCGTGGCTGGG ACTITCTGGAATGGCTGAGGCTAGAAATTGCACCA----AAACATTATTTGAAGTGGC **AATTGAGTGGTGAAAAAGTTTGTTTAATTGGACATTCTATGGGTTCTCAGATTATCTTTT** 

661 769

709

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Matches Query Match Sequence

428

TTGGCTATGAACCCAATAAATGACGAGTGCTGCGTATGATTGGAGGCTTGCATATTTAG

Local

Similarity

3.0%;

Score 49.4; DB 12; Pred. No. 0.0004; Mismatches 161;

Conservative

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Indels Length 1701; 0 Other;

6

1701

B₽;

516 A; 317 C; 401 G; 467 T; 0 U;

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CC acyltransferase polypeptide can produce fatty acid esters and/or fatty CC acid thioesters such as triacylglycerols, diacylglycerols, waxesters, CC monoacylglycerols, phospholipids, glycolipids, lysolipids, waxesters, CC acylated carbohydrates and acylated amino acids. Also described: (1) a CC nucleotide sequence molecule (II) comprising at least one promoter region which functions in a host, where the promoter region is operably linked to at least one (I), which is operably linked to at least one (I), which is operably linked to at least one comprising (II) or the vector; (4) producing an CC translated region which functions in a host; (2) a vector comprising (II) (2); (3) a host cell comprising (II) or the vector; (4) producing an CC improved active membrane independent acyltransferase polypeptide, (CC comprising providing the above host cell culture and harvesting the host cell culture and harvesting the cell culture and harvesting the cell culture and recovering the host cell culture and harvesting the cell culture and polypeptide at least is an improved active membrane independent acyltransferase polypeptide; (5) a polypeptide obtained by the method in CC independent acyltransferase polypeptide; (6) an oligonucleotide comprising the above polypeptide and a stabiliser. The nucleic acid CC comprising the above polypeptide are useful in producing structured CC injude or fat-soluble molecules, in removing undestrable fat or in CC modifying lipids present in animal and plant raw material. The present or comprising the seemal interesting the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid residue of the membrane-spanning region has been deleted and/or substituted as compared to the original acyltransferase polypeptide, where the encoded active membrane independent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleotide sequence encoding an acyltransferase polypeptide comprising least one membrane-spanning region. (I) encodes an improved active membrane independent acyltransferase polypeptide in which at least one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleotide sequence encoding an improved acyltransferase polypeptide, useful for producing structured lipids or fat-soluble molecules, in removing undesirable fat or in modifying lipids in animal or plant raw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 12; SEQ ID NO 2;
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29-MAY-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present invention describes a nucleotide sequence (I) derived from
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2003SE-00000142.
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RESULT 11
ACG4431
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                                                                                                                                                                                               Query Match
Best Local S
Matches 162
                                                                                                                                                                                                                                                                                                                                                               The present invention describes an enzyme for catalysing (in an acyl-CoA-independent reaction) the transfer of fatty acids from phospholipids to diacylglycerol in the biosynthetic pathway for the production of triacylglycerol (TAG). The enzyme is designated as phospholipid:diacylglycerol acyltransferase (PDAT). The enzyme and the nucleotides encoding them are useful for producing TAG and/or TAG with uncommon fatty acids. The enzyme and the nucleotide are also useful for transforming any cell or organism in order to be expressed in this cell or organism and result in an altered, preferably increased oil content of this cell or organism. The present sequence encodes yeast (Saccharomyces
                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                               cerevisiae)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phospholipid:diacylglycerol acyltransferase enzymes in the biosynthetic pathway for triacylglycerol production and DNAs encoding them, useful for producing triacylglycerol, or for transforming any cell or organism to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dahlqvist
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875
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                                                                                                                                                                                                                                                                                              1986
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ATCTAGAAAGACGCGATAGGTACTTTACGAAGCTAAAGGAACAAATCGAACTGTTTCATC
                                 AATTGGAAGAGCGTGACCTTTACTTTCACAAGCTCAAGTTGACCTTTGAAACTGCTTTAA
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Pred. No. 0.00044;
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Query Match Best Local Similarity

3.0%; 49.2%;

Score 49.4; Pred. No. 0.

4; DB 3; 0.00044;

Length 1986;

Sequence

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RESULT 12
AAC64441
ID AAC64
                                     The present invention describes an enzyme for catalysing (in an acyl-Co independent reaction) the transfer of fatty acids from phospholipids to diacylglycerol in the biosynthetic pathway for the production of triacylglycerol (TAG). The enzyme is designated as phospholipid:diacylglycerol acyltransferase (PDAT). The enzyme and the nucleotides encoding them are useful for producing TAG and/or TAG with uncommon fatty acids. The enzyme and the nucleotide are also useful for transforming any cell or organism in order to be expressed in this cell or organism. The present sequence represents the yeast (Saccharomyces cerevisiae) PDAT gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-APR-1999;
10-JUN-1999;
07-FEB-2000;
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                                                                                                                                                                                                                                                                                                Claim 6; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dahlqvist A,
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10-JUN-1999;
07-FEB-2000;
The present invention describes an enzyme for catalysing (in an acyl-CoA-independent reaction) the transfer of fatty acids from phospholipids to diacyl-glycerol in the biosynthetic pathway for the production of triacyl-glycerol (TAG). The enzyme is designated as phospholipid:diacyl-glycerol acyl-transferase (PDAT). The enzyme and the nucleotides encoding them are useful for producing TAG and/or TAG with uncommon fatty acids. The enzyme and the nucleotide are also useful for
                                                                                                     Claim
                                                                                                                                     Phospholipid:diacylglycerol acyltransferase enzymes in the biosynthetic pathway for triacylglycerol production and DNAs encoding them, useful for producing triacylglycerol, or for transforming any cell or organism to
                                                                                                                                                                                                                             Dahlqvist
                                                                                                                                                                                                                                                                                                                             28-MAR-2000; 2000WO-EP002701
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)B; AAB24265.
                                                                                                                                                                                                                                                                                                                                                                                                                            phospholipid:diacylglycerol acyltransferase; triacylglycerol;
expressed sequence tag; fatty acid; oil content; ds.
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99EP-00111321.
2000US-0180687P.
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Best Local Sim
Matches 162;
  WPI; 2001-169010/17
P-PSDB; AAU00464.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lecithin:cholesterol acyltransferase-like; LCAT; sterol acyltransferase; acyl CoA:cholesterol acyltransferase-like; ACAT; plant oil; cooking oil; nutritional supplement; dairy product; food product; salad dressing; yeast; Arabidopsis thaliana; LCAT related open reading frame 1; LRO1; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-MAY-2001
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                                                                      Lassner M,
                                                                                                                                                                     30-AUG-1999;
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ilarity 49.2%;
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Pred. No. 0.00044;
D; Mismatches 161;
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CC and ACAT (acyl CoA; cholesterol acyltransferase-like; Assoli31-Assoli34)
CC and ACAT (acyl CoA; cholesterol acyltransferase-like; Assoli311-Assoli319).
CC A rat ACAT-like cDNA sequence (ASsoli05) is also described. The
CC polymucleotides encoding LCAT or ACAT are used to produce LCAT or ACAT
CC polymeptides. They can also be used in a recombinant construct to
CC transform a host cell (preferably of a plant) or a plant. The recombinant
CC construct is used to increase or decrease the sterol content of the host
CC cell or plant. It can be used to alter oil production of the cell or
CC plant, preferably by increasing it. The oil of the plant or the plant
CC itself is used as a food product, or as mutritional or dietary
CC supplements, or in pharmaceutical compositions for lowering cholesterol.
CC The oil can be used in foods e.g. margarine, butter, cooking oil, and
CC dressings e.g. salad dressings, mayonnaise, cheese, processed meat,
CC pasta, sauces, cereals, desserts, dips, baked goods, pastries,
CC pasta, sauces, cereals, desserts, dips, baked goods, pastries,
CC pasta, sauces, corsent and/or composition can also provide a plant
CC with tolerance to stress and insect damage
acyltransferase; enzyme; membrane-spanning region; active membrane independent acyltransferase; fatty acid ester; fatty acid thioester; triacylglycerol; diacylglycerol; monoacylglycerol;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid encoding plant lecithin:cholesterol acyltransferase-like or acyl (coenzyme A) CoA:cholesterol acyltransferase-like polypeptides, for modifying the sterol content and oil production of plants.
                                                                                                                                                                                                         ADF47816 standard;
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                                                                                     Yeast acyltransferase
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Pred. No. 0.00044;
0; Mismatches 161;
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Saccharomyces cerevisiae
                                                                                                                       phospholipid; glycolipid; lysolipid; waxester; acylated carbohydrate;
acylated amino acid; structured lipid; fat-soluble molecule; yeast; g
                                                                                                                                gene;
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04-DEC-2003

28-MAY-2003; 2003WO-SE000870

29-MAY-2002; 29-MAY-2002; ; 2002SE-00001581. ; 2002US-0383889P. ; 2003SE-00000142.

(SCAN-) SCANBI SCANDINAVIAN BIOTECHNOLOGY RES A

Ą Α, Lindqvist Y, Banas A;

2004-053268/05 DB; ADF47818.

New nucleotide sequence encoding an improved acyltransferase polypeptide, useful for producing structured lipids or fat-soluble molecules, in removing undesirable fat or in modifying lipids in animal or plant raw

Claim 5; SEQ ID NO 1; 91pp; English

CC acid thioesters such as triacylglycerols, diacylglycerols, waxesters, cc acid thioesters such as triacylglycerols, diacylglycerols, waxesters, cc monoacylglycerols, phospholipids, glycolipids, lysolipids, waxesters, cc acylated carbohydrates and acylated amino acids. Also described: (1) a comcleotide sequence molecule (II) comprising at least one promoter region which functions in a host, where the promoter region is operably linked to at least one (II), which is operably linked to at least one for translated region which functions in a host; (2) a vector comprising (II) cc translated region which functions in a host; (2) a vector comprising (II) (2); (3) a host cell comprising (II) or the vector; (4) producing an cc improved active membrane independent acyltransferase polypeptide, comprising providing the above host cell culture and harvesting the host cell culture and recovering the host cell culture and harvesting the cc host cell culture and recovering the improved active membrane independent acyltransferase polypeptide obtained by the method in cell culture the polypeptide at least is an improved active membrane independent acyltransferase polypeptide and a stabiliser. The nucleic acid comprising the above polypeptide are useful in producing structured clipids or fat-soluble molecules, in removing undesirable fat or in codifying lipids present in animal and plant raw material. The present conditions is used in the exemplification of the present invention. amino acid residue of the membrane-spanning region has been deleted and/or substituted as compared to the original acyltransferase polypeptide, where the encoded active membrane independent nucleotide sequence encoding an acyltransferase polypeptide comprising least one membrane-spanning region. (I) encodes an improved active membrane independent acyltransferase polypeptide in which at least one The present invention describes a nucleotide sequence (I) derived from a a

Sequence 1986 B₽; 615 A; 361 C; 478 G; 532 T; 0 U; 0 Other;

Length 1986;

Query Match

ર્ 문 Ś Matches Local Similarity AATTGGAAGAGCGTGACCTTTACTTTCACAAGCTCAAGTTGACCTTTGAAACTGCTTTAA TTGGCTATGAACCCAATAAAATGACGAGTGCTGCGTATGATTGGAGGCTTGCATATTTAG 3.0%; <u>,</u> Score 49.4; DB 12; Pred. No. 0.00044; 0; Mismatches 161; Indels 6 Gaps 487 874 547

**ATCTAGAAAGACGCGATAGGTACTTTACGAAGCTAAAGGAACAAATCGAACTGTTTCATC** 934

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GenCore version 5.1

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4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

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## SUMMARIES

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Sequence 443, App	443,	443,	Sequence 443, App	443,	Sequence 17094, A	2813,	Sequence 12751, A	Sequence 15318, A	1376	Sequence 14, Appl	4019	1521,	Sequence 2485, Ap	170	41	4,	28	2439,	202	22	135	14,	13,	,-	Sequence 1, Appli	Sequence 1147, Ap	Description

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### ALIGNMENTS

RESULT 1 US-09-248-796A-1147

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Sequence 1147, Application US/09248796A

Patent No. 6747137

Patent No. 6747137

PATENTIANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
ITITLE OF INVENTION: NUCLEIC ACID AND ACID SEQUENCES RELATING TO C
ITITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR PILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR PILING DATE: 1998-08-13
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; OTHER INFORMATION: Identity of nucleotide sequences at the above US-09-248-796A-1147
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SEQ ID NO 1147
LENGTH: 2106
TYPE: DNA
ORGANISM: Candida albicans
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Best Local Similarity
Matches 173; Conserv
1121
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                                                                                                                  TTGCCCATTCAATGGGTAATAATGTCTTCAGATACTTTCTGGAATGGCTG-----AGGC 628
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Pred. No. 0.00019;
0; Mismatches 183;
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CURRENT FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
NUMBER OF SEQ ID NOS: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bult et al. TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanocoo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
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                                  NAME/KEY: misc_feature
LOCATION: (163385)..(163385)
OTHER INFORMATION: n equals
                                                                   NAME/KEY: misc_feature
LOCATION: (148948)..(148948)
OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
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NAME/KEY: misc_feature
LOCATION: (191989)..(191989)
OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
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LOCATION: (231980)..(231980)
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LOCATION: (871619)..(871619)
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Sequence 1, Application US/09692570

Patent No. 6797466

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Best Local Sim:
Matches 118;
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LOCATION: (1603734)...(1603734)
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LOCATION: (1637998)...(1637998)
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APPLICANT: Bult et al
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LOCATION: (1470091)..(1470091)
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LOCATION: (1569020)..(1569020)
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SOFTWARE: PatentIn version 3.1 SEQ ID NO 1
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TITLE OF INVENTION:
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                                                                                                            FEATURE:
NAME/KEY: misc feature
NAME/KEY: misc feature
(148948)..(148948)
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LOCATION: (28257)..(28258)
OTHER INFORMATION: n equals
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LOCATION: (98159)..(98159)
OTHER INFORMATION: n equals
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NAME/KEY: misc_feature
LOCATION: (84808)...(84808)
OTHER INFORMATION: n equals
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LOCATION: (28272)..(28222)
OTHER INFORMATION: n equals
        NAME/KEY: misc feature
LOCATION: (191989)..(191989)
OTHER INFORMATION: n equals
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NAME/KEY: misc_feature
LOCATION: (163385)..(163385)
OTHER INFORMATION: n equals
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NAME/KEY: misc_feature
LOCATION: (103998)..(103998)
OTHER INFORMATION: n equals
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LOCATION: (98343)..(98343)
OTHER INFORMATION: n equals
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LOCATION: (98266)..(98266)
OTHER INFORMATION: n equals
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LOCATION: (98239)..(98239)
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LOCATION: (98120)..(98120)
OTHER INFORMATION: n equal
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LOCATION: (84773)...(84773)
OTHER INFORMATION: n equals
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NAME/KEY: misc feature

COATION: (559167)...(5:
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NAME/KEY: misc_feature
LOCATION: (682442)..(682442)
OTHER INFORMATION: n equals
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NAME/KEY: misc_feature
LOCATION: (674435)..(674435)
OTHER_INFORMATION: n equals
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LOCATION: (657203)..(657203)
OTHER INFORMATION: n equals
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LOCATION: (657081)...(657081)
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LOCATION: (622708)..(622708)
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LOCATION: (559241)..(559241)
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LOCATION: (319226)..(319226)
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LOCATION: (312993)..(312993)
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LOCATION: (234814)..(234814)
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LOCATION: (234220)..(234220)
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LOCATION: (234187)...(234187)
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LOCATION: (231980)..(231980)
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LOCATION: (312837)..(312837)
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LOCATION: (309418)..(309418)
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LOCATION: (309398)..(309398)
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LOCATION: (191995)..(191995)
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LOCATION: (600992)..(600992)
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Best Local Similarity 47.8%;
Matches 118; Conservative
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OTHER INFORMATION: n equals a, t
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NAME/KEY: misc_feature
LOCATION: (741684)...(741684)
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LOCATION: (1349473)..(1349473)
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LOCATION: (1084830)..(1084830)
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LOCATION: (1313224)..(1313224)
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LOCATION: (871619)..(871619)
OTHER INFORMATION: n equals
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NAME/KEY: misc_feature
LOCATION: (855539)..(855539)
OTHER INFORMATION: n equals
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NAME/KEY: misc_feature
LOCATION: (779676)..(779676)
OTHER INFORMATION: n equals
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LOCATION: (779455)...(779455)
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LOCATION: (1310988)..(1310988)
OTHER_INFORMATION: n equals a,
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LOCATION: (1130881)..(1130881)
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                                      1220397
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AGTATTT 576
                                      ATTTAATAAGCTTTACTATCTTTATGCAAATGCAAAATAATTCCTTAATTTTCCTATTTT
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                                                             CTTTCACAAGCTCAAGTTGACCTTTGAAACTGCTTTAAAACTCCGTGGCGGCCCCTTCTAT
                                                                                       AGGAGCTATTAACAACCTTGAAGAAATATTAAATAATAAAATACAAAATACAGTGAATAA
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/148,934
PRIOR FILING DATE: 1999-08-12
PRIOR APPLICATION NUMBER: US 60/148,933
PRIOR FILING DATE: 1999-08-12
PRIOR APPLICATION NUMBER: US 60/177,047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 06618-686001
CURRENT APPLICATION NUMBER: US/09/639,207
CURRENT FILING DATE: 2000-08-14
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PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 2000-05-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: AN ANIMAL MODEL OF POLYGLUTAMINE TITLE OF INVENTION: TOXICITY, METHODS OF USE, AND MODULATORS TITLE OF INVENTION: TOXICITY
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ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                APPLICANT: DORNER, F.
APPLICANT: SCHELFLINGER, F.
APPLICANT: FALKMER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                           COUNTRY: USA
ZIP: 22313-0299
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Similarity 56.2%;
73; Conservative
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FastSEQ for Windows Version 4.0
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                                                                                                                                                              1800 Diagonal Road,
 PatentIn Release #1.0, Version #1.25
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UMBER: US 60/205,720
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Pred. No. 0.045;
"" matches 57;
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RESULT 6
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                                                    GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTIC
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
                                                                                                                                                                                                                                                       Sequence 13539, Application US/09949016 Patent No. 6812339
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FILING DATE:
APPLICATION NUMBER: EP 91 114
PILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAMB: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 3047
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 899149
INFORMATION FOR SEQ ID NO:
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LENGTH: 7218 base pairs
TYPE: nucleic acid
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CLONE: pTZgpt-
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TELEFAX: (703)683-4109
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FILING DATE: 2000-10-03
APPLICATION NUMBER: 60/231,498
FILING DATE: 2000-09-08
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Pred. No. 0.33;
90; Mismatches 144;
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US-09-806-708B-22/c
; Sequence 22, Application US/09806708B
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(314798)
OTHER INFORMATION: n = A,T,C
US-09-949-016-13539
                                                                                                                                                                                                                                                                                                            US-09-806-708B-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PATENT NO. 6784342

GENERAL INFORMATION:
APPLICANT: The University of British Columbia
TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
FILE REFERENCE: 4810-58741
CURRENT EILING DATE: 2001-04-03
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 60/147,133
PRIOR FILING DATE: 1999-08-04
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin version 3.0
SEQ ID NO 22
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13539
LENGTH: 314798
TYPE: DNA
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
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Local Similarity 46.7%;
hes 122; Conservative
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                                                                                                                                                              488 AATTGGAAGAGCGTGACCTTTACTTTCACAAGCTCAAGTTGACCTTTGAAACTGCTTTAA 547
                                                                                                                                                                                                                                       Similarity
                                                                    AACTCCGTGGCGGCCCTTCTATAGTATTTGCCCCATTCAATGGGTAATAATGTCTTCAGAT
                                                                                                                  RHHTRTCRRTKYNNNNNNARTVYWYHHAARRWMNAWTRTNNNNNNNNNNNACRNTRTWWA
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                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                               consensus sequence of A.t., L.a.,
                                                                                                                                                                                                                                       9.68;
                                                                                                                                                                                                            3%; Score 38.2; DB 4;
b; Pred. No. 0.13;
280; Mismatches 405;
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Pred. No. 4.5;
0; Mismatches 139;
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                                                                                            ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2027
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US-09-949-016-2027
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                                                                                                                                                         PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FBBUSEQ for Windows Version 4.0
SEQ ID NO 2027
LENGTH: 4465
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
Query Match
Best Local Similarity
Matches 67; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
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o. 6812339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TMWWRHWNNNNTDTRYYWWWKRWARBTTTVYDSMCNAKSMWRGNNWRAMKMWWAANNDAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WYAYMHMHKKGKAAWTNNKTABRDDHBAHVKTYWYWRYDY 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGTATTTTGCATATATGGTGCTCATCTAAAGACAGAGGTT 1245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGTATCATGATGACCCTGTTTTTAATCCTCTGACTCCTTGGGAGAGACCACCTATAAAAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NNNNNNKAWYYRTKTVAWCNNRYYYDTAVWTBKRNYKYCYAYBWYYBMYMGKHHWBWWRR
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    Conservative
                   2.3%;
Score 37.6; DB 4; Length 4465; Pred. No. 0.52; O; Mismatches 49; Indels 0
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OF DETECTION AND USES THEREOF
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APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
ITILE OF INVENTION: EST8 and Encoded Human Proteins.
FILE REFERENCE: GENSET 0.54PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 2439
LENGTH: 581
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US-09-621-976-2439/c
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                              APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 2813
LENGTH: 832
TYPE: DNA
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Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
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                                                                                                                                                                                                                          APPLICANT: Jobert, S.
                                                                                                                                                                                                                                               APPLICANT: Dumas Milne Edwards, J.B.
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NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                ORGANISM: Homo sapiens
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GENERAL INFORMATION:
APPLICANT: KESHI ET AL
APPLICANT: KESHI ET AL
TITLE OF INVENTION: PROBE FOR DIAGNOSING INFECTIOUS DIA
FILE REFERENCE: 19036/33767
CURRENT APPLICATION NUMBER: US/08/809,254A
CURRENT FILING DATE: 1997-05-16
PRIOR APPLICATION NUMBER: PCT/JP95/02036
PRIOR APPLICATION NUMBER: JP 236348
PRIOR FILING DATE: 1994-09-30
PRIOR FILING DATE: 1994-09-30
NUMBER OF SEQ ID NOS: 9
NUMBER OF SEQ ID NOS: 9
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; LOCATION: 235..399
US-09-621-976-2813
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                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Synthetic probe US-08-809-254A-4
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                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 4
LENGTH: 5829
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
                                                                                                                                                                                                                                    Query Match 2.1%;
Best Local Similarity 49.2%;
Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08809254A Patent No. 6660852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn version 3.1
                                                                                                               325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            363 TCCAGGTTACATAACAGGTCCTCTTTCTACTGTCTGGAAAGAGTGGCTTAAGTGGTGTGT 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98
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                                                                                                                                                         AACGCATACTATTAAGCTTTTTCAAGACCTAATAATATGCGCTGTTCTGATTTGAAAGAC
                                                                                                                                                                                               AAAACATTATTTGAAGTGGCTTGATCAGCATATCCATGCTTATTTCGCTGTTGGAGCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGAGTTTGGTATAGAAGCAAATGCAATTGTCGCTGTTCCATACGATTGGAGATTGTCACC 482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ARSAKRCCYSCSWGAMSWKYMWRMWRWRGWATGAGMKAWRASCMMRRKYAGKSKTSYKSM
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TGTTTCTGAGGGAACTGCTCGGTTGTTGTCCAATTCTTTTGCGTCGTCATTGTGGCTTAT 821
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                                                                                                                                                                                                                                    Score 35; DB (
Pred. No. 4.6;
0; Mismatches
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US-09-949-016-17057

US-09-949-016-17057, Application US/09949016

; Sequence 17057, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:
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US-08-961-527-41/c
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                                                                                                                                                 RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 41, Application US/08961527
Patent No. 6420135
GENERAL INFORMATION:
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 9828 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 3
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TITLE OF INVENTION: Strep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: dou
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STATE: Maryland
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       762
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             642 AAAACATTATTTGAAGTGGCTTGATCAGCATATCCATGCTTATTTCGCTGTTGGAGCTCC 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92;
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Similarity 49.2%;
92; Conservative
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                                                                                                                                                                                                                                                                                                                    GCCATTT 828
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                                                                                                                                                                                                                                                    GCCATTT 3928
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9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (301) 309-8504
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Pred. No. 6.6;
0; Mismatches
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; OTHER INFORMATION: Description of Artificial Sequence: synthetic; OTHER INFORMATION: nucleic acid sequence US-09-710-279-2485
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US-09-710-279-2485
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; ORGANISM: Human
US-09-949-016-17057
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES AS;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILLING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PRILING DATE: 2000-10-20
PRIOR FILLING DATE: 2000-10-20
PRIOR RILING DATE: 2000-10-30
PRIOR RILING DATE: 2000-10-30
PRIOR RILING DATE: 2000-10-30
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILLING DATE: 2000-09-08
PRIOR FILLING DATE: 2000-09-08
PRIOR FILLING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/710,279
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2485
LENGTH: 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2485, Application US/09710279
Patent No. 6703492
GENERAL INFORMATION:
                                                                                                                               Query Match
Best Local Similarity
Matches 84; Conserv
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SEQ ID NO 17057
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 2.1%;
Best Local Similarity 51.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
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SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                TYPE: DNA
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    CATTTTTCTGGGGGTGCTGCAAAGAAAAAATAAGCGCGTATACCACTGTGATGAAGAGGAA
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ilarity 50.6%;
Conservative
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                                                                                                                               Score 34.8; DB
Pred. No. 0.95;
0; Mismatches
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Pred. No. 44;
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Sequence 1521, Application US/09134001C

Patent No. 6380370

GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
ITILE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
ITILE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
ITILE OF INVENTION: UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
ITILE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
ITILE OF INVENTION UNUMBER: US/09/134,001C
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US/09/064,964
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 1521
LENGTH: 477
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1521
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Search completed: November 9, 2005, 01:39:27 Job time : 313 secs
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US-09-134-001C-1521
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1: /cgn2 6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_***

4: /cgn2_6/ptodata/2/pubpna/US06_****
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# SUMMARIES

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Sequence 137717,	US-10-425-115-137717	21	924	11.8	193	4
Sequence 134518,	US-10-424-599-134518	19	528	13.2	215.8	ω
Sequence 16008, A	US-10-424-599-16008	19	1760	15.4	252.6	2
Sequence 76086, A	US-10-437-963-76086	20	1719	36.1	591.8	1
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	ence 1, App ence 114201 ence 665799 ence 324, Ap	e 38267, e 38278, e 38278, e 21, Ap e 718981 e 718982 e 718983	Sequence 24163, A Sequence 24169, A Sequence 38293, A Sequence 31256, A Sequence 18841, A Sequence 65323, A Sequence 78, Appl	e 6824, e 56537, e 23539, e 23539, e 226, f e 198, f e 198, f e 1107, f e 11	Sequence 93909, A Sequence 17331, A Sequence 57573, A Sequence 45, Appl Sequence 57116, A Sequence 61794, A Sequence 93908, A Sequence 13, Appl

### ALIGNMENTS

US-10-437-963-76086

Sequence 76086, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:

APPLICANT: La ROSA, Thomas J. APPLICANT: Kovalic, David K. APPLICANT: Zhou, Yihua

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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement; FILE REFERENCE: 38-22(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963; CURRENT FILING DATE: 2003-05-14; NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 76086
LENGTH: 1719
TYPE: DNA
ORGANTS**
                                      US-10-437-963-76086
  Query Match
                                                  FEATURE: OTHER INFORMATION: Clone ID: PAT_MRT4530_76111C.1
  36.1%; Score 591.8; DB 20;
Length 1719;
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US-10-424-599-16008
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APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 16008
LENGTH: 1760
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 16008, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La ROSA Thomas J
APPLICANT: Kovalic David K
                                                                                                                                      Best Local Similarity
                                                                                                                                                  Query Match
                                                                                                                       Matches 309;
                                                                                                                                                                                      TYPE: DNA
ORGANISM: Glycine max
PERATURE:
FRATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_114461C.1
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   CTGGATCATTÁCGGATGTCGTTTATGAGTTTGAAGGATCTCTAATCTCAAGGTCAGGGAA
                               TTGGATCACGGATATCATTTACGAAACTGAAGGTTCCCTCGTGTCAAGGTCTGGAAC 1346
                                                                                       TCATCTAAAGACAGAGGTTGGTTATTACTTTGCCCCAAGTGGCAAACCTTATCCTGATAA 1286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGGGTTAAGTACATAACCTTTTATGAAGACTCTGAGAGCATTCCGGGGAAGAGAACCGC
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                                                                                                                      Conservative
                                                                                                                                    15.4%;
                                                                                                                    Score 252.6; DB 1
Pred. No. 2.9e-67;
0; Mismatches 94
                                                                                                                                                    DB 19;
                                                                                                                                                  Length 1760
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_9247C.1
US-10-424-599-134518
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US-10-424-599-134518
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Best Local S
Matches 264
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APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (5.323)8
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 134518
LENGTH: 528
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APPLICANT: Kovalic David K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Glycine
                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                         CATCACAGAATTGGATCCAGGTTACATAACAGGTCCTCTTTC-TACTGTCTGGAAAGAGT
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GGATTAAGTGGTGTATTGAATTTGGCA
                                 GGCTTAAGTGGTGTGTTGAGTTTGGTA 433
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80.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                           Score 215.8; DB 1
Pred. No. 4.4e-56;
0; Mismatches 62
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US-10-425-115-93907
US-10-425-115-93907; Application US/10425115
; Sequence 93907, Application US/10425115
; Publication No. US20040214272A1
; APPLICANT: LA ROSA, Thomas J.
; APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yihua
APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and
TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
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US-10-425-115-137717
                                     US-10-425-115-93907
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LENGTH: 924
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Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
                                                                                                                 NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 93907
LENGTH: 848
TYPE: DNA
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Matches
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                                                                           ORGANISM: Zea mays FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Zea mays
                                                      OTHER INFORMATION: Clone ID: MRT4577_185630C.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Clone ID: MRT4577_57075C.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity hes 229; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               299 AAACAGACCATCCCGAGTGTAAGTCACGGCCTGACAGTGGTCTTTCAGCCATCACAGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         239 CTAAGCTTCTTTCTGCTGTCAACTGCTGGTTTAAGTGTATGGTGCTAGATCCTTATAATC
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79.2%;
11.4%;
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Pred. No. 8.6e-49;
0; Mismatches 60
Score 187.8;
                                                                                                                                                                                                                                                                                and Other Molecules Associated With
  BG
  21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 924;
Length 848;
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Sequence 93909, Application US/10425115

| Sequence 93909, Application No. US20040214272A1
| GENERAL INFORMATION:
| APPLICANT: LA ROSS, Thomas J.
| APPLICANT: Kovalic, David K.
| APPLICANT: Kovalic, David K.
| APPLICANT: Zhou, Yihua APPLICANT: Cao, Yongwei |
| TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With |
| TITLE OF INVENTION: Plants |
| FILE REFERENCE: 38-21(5322)B |
| CURRENT APPLICATION NUMBER: US/10/425,115 |
| CURRENT APPLICATION NUMBER: US/10/425,115 |
| CURRENT FILING DATE: 2003-04-28 |
| NUMBER OF SEQ ID NOS: 369326 |
| SEQ ID NO 93909 |
| LENGTH: 1383 |
| TYPE: DNA |
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US-10-425-115-93909
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Best Local Similarity
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                                              GAGATTGTCACCAACCAAATTGGAAGAGCGTGACCTTTACTTTCACAAGCTCAAGTT 527
                                                                                                                                                                 TAAGTGGTGTGTTGAGTTTGGTATAGAAGCAAATGCAATTGTCGCTGTTCCATACGATTG 470
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GAGACTGCCCCCATCAATGCTTGAGGAGAGAGATCTGTACTTTCACAAATTAAAGTT 992
                                                                                                                      CAAATGGTGTGTAGAGTTTGGCATTGAAGCTAATGCAATTATCGCTGTTCCCGTATGATTG
                                                                                                                                                                                                                                                   TTGGATCCAGGTTACATAA-----CAGGTCCTCTTTCTACTGTCTGGAAAGAGTGGCT 410
                                                                                                                                                                                                                                                                                                                                                                            CAGACAGACCATCCCGAATGCAAATCAAGGCCTGATAGTGGTCTTTCTGCAATTACAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                        CAAACAGACCATCCCGAGTGTAAGTCACGGCCTGACAGTGGTCTTTCAGCCATCACAGAA 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AATGCTTGAGGAGAGATCTGTACTTTCACAAATTAAACAGGATCAGTAAGAGT 681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAAATTGGAAGAGCGTGACCTTTACTTTCACAAGCTCAAGTTGACCTTTGAAACT 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 173.8; DB 21;
Pred. No. 1.1e-42;
0; Mismatches 62;
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RESULT 7

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; OTHER INFORMATION: Clone US-10-424-599-57573
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                                              APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Can Vinua
APPLICANT: Can Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 57573
LENGTH: 380
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
FEAT
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANY: La Rosa Thomas J
APPLICANY: Kovalic David K
APPLICANY: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NO 17331
LENGTH: 1433
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Best Local Similarity
Matches 186; Conserv
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LOCATION: (1)...(1433)
OTHER INFORMATION: unsure at all n locations
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ORGANISM: Glycine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     963 TAACATTGAAATTCCTTCCACTAGCG------TACAGAAACAGC 1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGAACTAGCAGATGGGACTCTTTTCAAAGCAATAGAAGACTATGACCCAGATAGCAAGAG 1121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GATGTTACACCAGTTAAAGAAGTT 1145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATATCACTGTGATGAGCAGGAGTTTAAGACAAACTTATCTGGGTGGCCAACAAAAATAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTCTTGTACCTGTTAGAGAAGTT 312
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70.5%;
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                              ID: PAT_MRT3847_22C.1
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Pred. No. 4.5e-26,
0; Mismatches 5'
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RESULT 9
US-10-883-760-45

Sequence 45, Application US/10883760

Publication No. US20050035174A1

GENERAL INFORMATION:
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APPLICANT: Yadav, Narendra
APPLICANT: Zhang, Hongxiang
TITLE OF INVENTION: ACYLTRANSFERASES FOR ALTERATION OF POLYUNSATURATED FATTY ACIDS
TITLE OF INVENTION: AND OIL CONTENT IN OLEAGINOUS YEASTS
FILE REFERENCE: CL2302 US NA
CURRENT APPLICATION NUMBER: US/10/883,760
CURRENT FILING DATE: 2004-07-06
NUMBER OF SEQ ID NOS: 86
SOFTWARE: Patentin version 3.2
SEQ ID NO 45
LENGTH: 2326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 176; Conserv
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Best Local Similarity 61.2
Matches 167; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: (2271)..(2271)
OTHER INFORMATION: n is a, c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Yarrowia lipolytica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                    1076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1413
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1256 GATATGGAGGAGGACCCCAACTGGGTCAATGACCATATTGAATCCTTTGTCGACATTT 1315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 AAAGAATAGGACGGTAACTACTATGCTCCTAGCCGTGAGCCCTACCCTGAACACTGGATC 168
                                                                                         CGGGCCATTCCATGGGCTCCCAGGTCATCTTCTACTTCATGAAGTGGGCTGAGGCCGAGG 1255
                                                                                                                                                                                   CCAAGCTCAAAGCTTCAATCGAAGAGACTAAGCGTATGACAGGTGAGAAGACAGTTCTGA 1195
                                                                                                                                                                                                                                    ACAAGCTCAAGTTGACCTTTGAAACTGCTTTAAAACTCCGTGGCGGCCCTTCTATAGTAT 574
                                                                                                                                                                                                                                                                                                                              CTGTTCCATACGATTGGAGATTGTCACCAACCAAATTGGAAGAGCGTGACCTTTACTTTC 514
                                                                                                                                                                                                                                                                                                                                                                           TGTGGAACAAGCTGCTCGAGAACCTGGCTGTTATTGGATACGATACGGATACAATGTCTG 1075
                                                                                                                                                                                                                                                                                                                                                                                                                          TCTGGAAAGAGTGGCTTAAGTGGTGTGTTTGAGTTTGGTATAGAAGCAAATGCAATTGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGGAAGCGACGTACATGTGGAACTAAATGTTG 1504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAGCAGAAACAGGCTTGGTCCGGATGTGCACATATACACAAGCCCCACCGTGTGAGCACG 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTGCAAGAATTGGCTCGGACCTAAAGTTAACATA-ACAATGGCTCCCCAGCCAGAACACG 1471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATCACGGATATCAT-TTACGAAACTGAAGGTTCCCTCGTGTCAAGGTCTGGAACTGTGGT 1352
                                       TTGCACCAAAACATTATTTGAAGTGGCTTGATCAGCATATCCATGCTTATTTCGCTGTTG
                                                                                                                         TTGCCCATTCAATGGGTAATAATGTCTTCAGATACTTTCTGGAATGGCTGAGGCTAGAAA 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAGGGTCAGATGTTCACCTTAAATTGGATGTGG 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGAGGGAACCCTGTATCCATAGC - CGCCATGAGACGGCGCCATACTTATCCCTTTTCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.1%; Score 68; DB 22; Length 2326;
49.4%; Pred. No. 2.1e-09;
ative 0; Mismatches 180; Indels
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Pred. No. 3.2e-11;
0; Mismatches 103;
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APPLICANT: LA ROBA, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 61794
LENGTH: 962
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                                                                                  ; OTHER INFORMATION: Clone ID: MRT4577_15634C.1 US-10-425-115-61794
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules an
TITLE OF INVENTION: Plants
FILE REPERENCE: 38-21 (5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-425-115-57116
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Best Local S
Matches 68
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 61794, Application US/10425115 Publication No. US20040214272A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 57116
LENGTH: 369
TYPE: DNA
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                                        Query Match
                                                                                                                                           TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: unsure
LOCATION: (1)..(369)
OTHER INFORMATION: unsure at all n locations
FEATURE:
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                                                                                                                          FEATURE:
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  Local Similarity
nes 60; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 3.4%;
Local Similarity 78.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           298 CAAACAGACCATCCCGAGTGTAAGTCA 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAGATAGACCATCCCGAATGCAAGTCA 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTAAGCTTCTTTCTGCTGTCAACTGCTGGTTTTAAGTGTATGGTGCTAGATCCTTATAAT 297
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                     3.1%;
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Score 51; DB 21;
Pred. No. 0.00025;
0; Mismatches 15;
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Pred. No. 2.4e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                          DB 21; Length 962;
                                                                                                                                                                                                                                                                                                                               and Other Molecules Associated With
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      Indels
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APPLICANT: KASCEMI-ESFARJANI, PARSA
APPLICANT: KASCEMI-ESFARJANI, PARSA
APPLICANT: BENZEY, SEYMOUT
TITLE OF INVENTION: AN ANIMAL MODEL OF POLYG
TITLE OF INVENTION: TOXICITY
FILE REFERENCE: 06618-686001
CURRENT APPLICATION NUMBER: US/10/465,217
CURRENT FILING DATE: 2003-06-18
PRIOR APPLICATION NUMBER: US/9/639,207
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: US 60/148,934
PRIOR FILING DATE: 1999-08-12
PRIOR FILING DATE: 1999-08-12
PRIOR FILING DATE: 1999-08-12
PRIOR APPLICATION NUMBER: US 60/177,047
PRIOR APPLICATION NUMBER: US 60/205,720
PRIOR FILING DATE: 2000-05-19
PRIOR FILING DATE: 2000-05-19
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US-10-465-217-13/c
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; OTHER INFORMATION: US-10-465-217-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
US-10-425-115-93908
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Best Local Similarity
Matches 50; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Nucleic Acid Molecules
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 93908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 93908, Application US/10425115 Publication No. US20040214272A1 GENERAL INFORMATION:
                                                                                                                                    SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Clone ID: MRT4577_185631C.1 -10-425-115-93908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 374
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
                                                                                                                                                     NUMBER OF SEQ ID NOS: 69
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: La Rosa, Thomas J. APPLICANT: Kovalic, David K.
                                     TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                          LENGTH: 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          321 GTCACGGCCTGACAGTGGTCTTTCAGCCATCACAGAATTGGATCCAGGTTACATAACAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGGAGCTTGATAAA 1629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTTAAGTACATAACCTTTTATGAAGACTCTGAGAGACATTCCGGGGAAGAGAGAACCGCAGTC 1614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGGAGCTCGATAAA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhou, Yihua
Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTGAAGTACATAACCTACTATGAGGATGCTGAAAGTCTTCCAGGATGGAGAACAGCAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/10465217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 44; DB 2
Pred. No. 0.021
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POLYGLUTAMINE
OF USE, AND MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.021;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AND MODULATORS OF POLYGLUTAMINE
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RESULT 15
US-10-424-599-56537
; Sequence 56537, Application US/10424599
; Publication No. US20040031072A1
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US-10-719-993-6824
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CURRENT APPLICATION NUMBER: US/10/719,993
CURRENT FILING DATE: 2003-11-24
NUMBER OF SEQ ID NOS: 55342
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6824
LENGTH: 325446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6824, Application US/10719993
Publication No. US20040265849A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPH.
TITLE OF INVENTION: ALZHEIMER'S DISE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 2.4%;
Best Local Similarity 46.7%;
Matches 122; Conservative
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Best Local Similarity
Matches 73; Conserve
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(325446)
OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
                                                                                                                    142542
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                                                                                                                    GGTGAATCTTTGCACATTACT 142562
                                                                                                                                                                                          TCTCAAGGGGGCTCTTTTGTACTGAAGTGTTTTTATTTACTTTAATGTAAGCATGTGCCAT 142541
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GENETIC POLYMORPHISMS ASSOCIATED WITH
ALZHEIMER'S DISEASE, METHODS OF DETECTION
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Pred. No. 1.1;
0; Mismatches
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GENERAL INFORMATION:
APPLICANT: La ROSA Thomas
APPLICANT: Kovalic David

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APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 56537
LENGTH: 1545
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_22062C.1
US-10-424-599-56537
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Search completed: November 9, 2005, 04:41:24 Job time: 1395 secs
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                                                                                                     1076 TTGGCCGTCTCATGCCATCTCTTATGTACT 1105
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                                                                                                                                  685 TTCGCTGTTGGAGCTCCTCTTCTTGGTTCT 714
                                                                                                                                                                                                                                    625 AGGCTAGAAATTGCACCAAAACATTATTTGAAGTGGCTTGATCAGGATATCCATGCTTAT 684
                                                                                                                                                                                                                                                                                                    956 TCTATTTTTTTGGTGCAACAGTTGGTTTTAGTATATCTTAATAACTTGGGACAAATAGCTG 1015
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Maximum Match 100%
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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CK939714
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1 NF097C07I
AU306500
SCSGFL403
SCEPRZ308
SCEPRZ308
PAM01-25m
Y014D01 P
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122.4	122.4	122.4	123.8	126.6	133.4	133.4	134.8	135.2	137	159	160	160.2	165.6	167.6	168.6	176.8	180.4	182.2	185	189.2
7.5	7.5	7.5	7.5	7.7	8.1	8.1	8.2	8.2	8.3	9.7	9.8	9.8	10.1	10.2	10.3	10.8	11.0	11.1	11.3	11.5
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### ALIGNMENTS

VERSION KEYWORDS LOCUS DEFINITION RESULT 1 CL949010 Ś 밁 S ORIGIN COMMENT REFERENCE FEATURES SOURCE ACCESSION Query Match Best Local Sim Matches 1026; TITLE JOURNAL. AUTHORS ORGANISM source 108 168 GTGGTCGATCCTTGACTGTCCATACACTCCGTTGGACTTCAATCCGCTCGACCTCGTATG Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676 Ma,L., Wangc,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M., Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L., Wong,G.K.S., Deng,X.W. and Wang,J.

An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis

Unpublished (2004) Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 1719) 1719 bp DNA linear GSS 21-SEP-2004 OBIFS002788 Oryza Bativa Express Library Oryza Bativa (indica cultivar-group) genomic, genomic survey sequence.
CL949010 Class: exon-trapped Rice genomic sequence. Email: chenchen@genomics.org.cn CL949010.1 GI:52361019 Similarity CGACTACTCGAAGCTATCGGGTATAATCATTCCGGGATTTGCGTCGACGCAGCTACGAGC 167 35.8%; llarity 65.0%; Conservative /organism="Oryza sativa (indica cultivar-group)"
/mol_type="genomic DNA"
/mol_type="genomic DNA"
/db_xref="ftaxon:39946"
/clone_llb="Oryza sativa Express Library"
/note="Oryza sativa exon trapped genomic sequence" Location/Qualifiers Score 587; DB 9; I Pred. No. 1.6e-164; D; Mismatches 385; Length 1719; Indels 168; sequences Gaps 182 227

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TCATCTAAAGACAGAGGTTGGTTAATTACTTTGCCCCAAGTGGCAAACCTTATCCTGATAA
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                                                                                                    CCCAGATAGCAAGAGGATGTTACACCAGTTAAAGAAGTTGTATCATGATGACCCTGTTTT
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Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
roside; euroside II; Brassicales; Brassicaceae; Arabidopsis.

E 1 (bases 1 to 596)
E 1 (bases 1 to 596)
S Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M.,
Akiyama,K., Enju,A., Oono,Y., Sakurai,T., Carninci,P., Kawai,J.,
Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A.,
Muramatsu,M., Hayashizaki,Y. and Shinozaki,K.
Large scale analysis of Arabidopsis full-length cDNA
Contact: Motoaki Seki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1152
                                                                                                                                                                                                                                                                    Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998).cDNA cleaved with BamHI and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et al., submitted for publication) digested with BamHI and SalI. This clone is in a modified pBluescript vector. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index _e.html) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki
Tel: 81-298-36-4359
Fax: 81-298-36-9060
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/organism="Arabidopsis t
/mol type="mRNA"
/db_xref="taxon:3702"
/clone="RAFFLL5-47-A08"
/tissue_type="mixture of
/lab_host="DH108"
                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                       Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr. Rockville, MD 20850,
                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Solanum.

1 (bases 1 to 946)

Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B. Generation of ESTs from abiotic stressed potato tissue
                                                                                                                                                                                                                                                                                                                                                                            946 bp mRNA li
EST705472 potato abiotic stress cDNA library
Clone POAB029 5' end, mRNA semianca
                                          Email: potato-array@tigr.org
Clones can be requested from the University of Arizona
Institute via http://genome.arizona.edu/orders/ .
Seq primer: CAG GAA ACA GCT ATG ACC.
                                                                                                                                                                  Unpublished (2003)
Other_ESTs: EST705470 EST705471 EST705473
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CK259394.1 GI:39816372
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Solanum tuberosum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTTGAGTTTGGTATAGAAGCAAATGCAATTGTCGCTGTTCCATACGATTGGAGATTGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GATCCAGGTTACATAACAGGTCCTCTTTCTACTGTCTGGAAAGAGTGGCTNAAGTGGTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTTGCGGTGGCCGAACTGCGGTGGAGGATGAGACCGAGTTTCACGGCGACTACTCGAAG 120
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                   Location/Qualifiers
1. .946
/organism="Solanum tuberosum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="RAFL15"
/note="Site_1: BamHI; Site_2: SalI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 484; DB 1;
Pred. No. 1e-133;
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                                                                                  Genomics
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Query Match
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                                                AAAGAAGTTGTATCATGATGACCCTGTTTTTAATCCTCTGACTCCTTGGGAGAGACACCACC 1196
                                                                                                                          AACCTTTTTCAAAGCCATAAAGAATTATGATCCTGACAGTGAAAGACTCTTTCACCTTTT
                                                                                                                                                                                                                                                 TGGAATGGAATGTGGATTCCCGACACAATTGTCCTTTTTCTGCTCGTGAAGTCTCTGACGG
                                                                                                                                                                                                                                                                                                                                                                                                                            TTCCACTAG-----CGTTACAGAAACAGCTCTAGTCAACATGAC 1016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGAGGAATATCAATCAAAATATTCTGGCTGGCCGACAAATATTATTAACATTGAAATTCC
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AAAAAAGTCTTACCATGATGATCCGATTTTAAATCCTCTAACACCTTGGGAAAGACCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="abiotic stress treated leaf and roc /lab host="PH10B-TonA" /clome_lib="potato abiotic stress cDNA library" /note="Twector: pCMVSport6.1; Site 1: EcoRI; Site supplier: Solanum tuberosum var. Kennebec plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              grown from cuttings on a 16hr light/8 hr dark cycle at 25 C for 3-4 weeks. Abiotic stress conditions were applied to four separate sets of plants. Set 1 involved saturation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           four separate sets of plants. Set 1 involved saturation the soil with 150 mM NaCl and tissues were harvested at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:4113"
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/cultivar="Kennebec"
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Pred. No. 1.1e-127;
0; Mismatches 253;
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ORIGIN

Matches

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ACCESSION
VERSION
KEYWORDS
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AUTHORS
TITLE
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CF844688
LOCUS
                                        ORIGIN
                                                                                                                                                                                                                                                                                  FEATURES
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   Query
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     Match
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FORWARD: BK reverse primer
BACKWARD: BK reverse primer
Plate: 029 row: F column: 13
Seg primer: BK reverse primer
High quality sequence stop: 752.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tyler, B.
Tyler, B. Not Published
Unpublished (2003)
Contact: Tyler B
Tyler lab
VBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CP844868 752 bp mRNA linear EST 30-OCT-200: psHB029xF13f USDA-IFAFS:Expression of Phytophthora sojae genes during infection and propagation_sHB Phytophthora sojae cDNA clone sHB029F13 5, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CF844688.1 GI:38060342
EST.
                                                                                                                                                                                                                                                                                                                                                                                                               Email: bmtyler@vt.edu
                                                                                                                                                                                                                                                                                                                                                                                                                             1880 Pratt Dr., Blacksburg, Tel: 540-231-7318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phytophthora sojae
Phytophthora sojae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 752)
                                                  /dev_stage="48 hr. post infection stage"
/lab host="Soybean plant"
/clone_lib="USDA-IFAFS:Expression of Phytophthora sojae
genes during infection and propagation_sHB"
/note="Vector: pBK-CMV; Site_1: EcoR1; Site_2: Xho1"
                                                                                                                                                                                         /mol_type="mxwar/db_xref="taxon:67593"
                                                                                                                                                  /tissue_type="mycelium"
/cell_line="P6497"
                                                                                                                                                                                                                      organism="Phytophthora
/mol_type="mRNA"
                                                                                                                                                                                       clone="8HB029F13"
   Score
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Citrus sinensis

Citrus sinensis

Citrus sinensis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Sapindales; Rutaceae; Citrus.

1 (bases 1 to 713)

1 (bases 1 to 713)

1 (bases 1, bask,J., Leslie,A., Xu,J., Cook,D. and Dandekar,A.

Analysis of peel specific genes in Citrus (2004)

Contact: Abhaya Dandekar, PhD

Contact: Abhaya Dandekar, PhD
                                                                         CAES Genome Facility UC Davis, Department of One Shields Ave, Davis,
                                                                                                                                                                                                                                                                                                                                                   CK939714 713 bp mRNA linear CGF1004746_F04 Developing fruit flavedo at 165 DAFB cDNA clone F1650002_IIF_F04 5', mRNA sequence.
CK939714 CK939714
                                  Tel: 530 752 7784
Fax: 530 752 8502
                                                                                                                                                                                                                                                                                                                                      CK939714.1
                     Email: amdandekar@ucdavis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCTTAAGTGGTGTTGAGTTTTGGTATAGAAGCAAATGCAATTGTCGCTGTTCCATACGA
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); Mismatches 131;
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568 ATAGTATTTGCCCATTCAATGGGTAATAATGTCTTCAGATACTTTCTGGAATGGCTGAGG
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                                                                                   TACTTTCACAAGCTCAAGTTGACCTTTGAAACTGCTTTTAAAACTCCCGTGGCGGCCCTTCT
                                                                                                                                         CTTAAGTGCATGACACTAGATCCTTACAATCAAACAGATAATCCCGAATGCAAGTCTCGA
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                                                           TATTTTCACAAACTAAAGTTGACATTTGAAACTGCCCTTAAACTTCGTGGTGGCCCCTCA
                                                                                                                                                                   TCCTCAGTGTGGAAAGAATGGGTTAAGTGGTGCGTTGAGTTTGGTATAGAGGCTAATTCA
                                                                                                                                                                                                                                                   TCTACTGTCTGGAAAGAGTGGCTTAAGTGGTGTGTTGAGTTTGGTATAGAAGCAAATGCA 447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone lib="Developing fruit flavedo at 165 DAFB"
/note="Organ: Fruit; Vector: pTriplEX2; Site 1: SfiIA;
Site_2: SfiIB; Developing citrus fruits were harvested
from trees growing in the 'Citrus variety collection' in
the Wolfskill experimental orchard located in Winters,
California (USA). Fruit was collected on October 22, 2003,
between 8 to 9 am and stored at 4C. The flavedo tissue was
dissected out of developing fruit (165 DAFB) and used to
isolate RNA using Trizol reagent from Invitrogen. The cONA
Library was constructed using the SMART cDNA library Kit
(Clontech). The primary library was en masse evicted and
plasmid DNA containing the cDNA library was isolated from
the resultant bacterial population. Plasmid DNA was then
transformed into ultra competent B coli cells (XL10 Gold;
Stratagene). Transformants were plated out on Q-trays
(2000 cfu/tray), picked using a Obot and archived in 384
well dishes "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="F1650002 IIF_F04"
/sex="Hermaphrodite"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       well dishes."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab host="XL10-Gold"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cultivar="Washington navel
/db_xref="taxon:2711"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Citrus sinensis"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        type="Falvedo"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 397; DB 7; 1
Pred. No. 1.7e-107;
0; Mismatches 145;
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Buell, C.R., Hart, A., Zismann, V., Karamych
Generation of ESTs from abiotic stressed |
Unpublished (2003)
Other_ESTs: EST705470 EST705472 EST705473
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Solanum tuberosum (potato)
Solanum tuberosum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/.
Seq primer: ATT TAG GTG ACA CTA TAG.
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The Institute for Genomic Research
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                   four separate sets of plants. Set 1 involved saturation of the soil with 150 mm NaCl and tissues were harvested at following application of the salt stress (leaves: 2hr, 6hr, 12hr, 1d, 2d, and 4d; roots:2hr, 6hr, 12hr, and 2d). Set 2 were grown under the standard conditions and then were water stressed by withdrawal of further watering applications. Drought stressed plants were harvested after cessation of watering (leaves: 3d, 5d, and 7d; roots:3d and 5d). Set 3 were grown under the standard conditions and then were cold stressed by placement at 4 C. Cold stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d, and 4d and heat-stressed by placement at 35 C. Heat stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, and 4d and heat-stressed at 2 hr, 6 hr, 12 hr, 1 d, and 4d and heat-stressed roots were harvested at 2 hr, 6 hr, 12 hr, 1 d, and 4d and 4d and heat-stressed roots were harvested at 2 hr, 6 hr, 12 hr, 1 d, and 4d a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab host="putato abiotic stress cDNA library" /clone_libe"potato abiotic stress cDNA library" /note="Vector: pCMVSport6.1; Site 1: EcoRI; Site 2: NotI; /note="Vector: pCMVSport6.1; Site 1: EcoRI; Site 2: NotI; supplier: Solanum tuberosum var. Kennebec plants were grown from cuttings on a 16hr light/8 hr dark cycle at 25 grown from extraines on a 16hr light/8 hr dark cycle at 25 grown from Salants Set 1 involved saturation of
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lab_host="DH10B-TonA"
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Query Match Best Local Si Matches 563;

Similarity

23.5%;

Score 386.2; DB 7; Pred. No. 3.1e-104; 0; Mismatches 203;

Length 7

25;

Gaps

Conservative

678 TGCTTATTTCGCTGTTGGAGCTCCTCTTCTTGGTTCTGTTGAGGCAATCAAATCTACTCT 737

root tissue"

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RESULT 7
CK260764
LOCUS
DEFINITION
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KEYWORDS
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CK260764.1 GI:39817742

EST.
Solanum tuberosum (potato)
Solanum tuberosum
Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
seterids; lamiids; Solanales; Solanaceae; Solanum.
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1 (bases 1 to 968)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Generation of ESTs from abiotic stressed potato tissue Unpublished (2003)
Other_ESTs: EST706843
                                                                                                                                                                                                                                                                                CK260764 968 bp mRNA linear I EST706842 potato abiotic stress cDNA library Solanum clone POAB552 5' end, mRNA sequence.
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Clones can be requested from the University of Arizona
Institute via http://genome.arizona.edu/orders/
Seq primer: ATT TAG GTG ACA CTA TAG.
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The Institute for Genomic Research
9712 Medical Center Dr, Rockville,
                                    GTGGTTGATGGGAACGCTGGACCTATAACTGGGGATGAGACGGTACCCTATCATTCACTC
                                                                                                                                                                                                 CATCTAAAGACAGAGGTTGGTTATTACTTTGCCCCAAGTGGCAAACCTTATCCTGATAAT
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    CTGGTTGAAGGAAACCCTGGTGCAACAAGTGGGGATGAGACGGTGCCATACCATTCCCTC
                                                                                                                           TGGATCATCACGGATATCATTTACGAAACTGAAGGTTCCCTCGTGTCAAGGTCTGGAACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G for 3-4 weeks. Abiotic stress conditions were applied to four separate sets of plants. Set 1 involved saturation of the soil with 150 mM NaCl and tissues were harvested at following application of the salt stress (leaves: 2hr. 6hr. 12hr. and 2d). Set 2 were grown under the standard conditions and then were water stressed by withdrawal of further watering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="potato abiotic stress cDNA library"
/note="Vector: pCMV5port6.1; Site 1: EcoR1, Site 2: Not1;
supplier: Solanum tuberosum var. Kennebec plants were
grown from cuttings on a 16hr light/8 hr dark cycle at 25
C for 3-4 weeks. Abiotic stress conditions were applied to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="abiotic stress treated leaf and
/lab_host="DH10B-TonA"
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/cultivar="Kennebec"
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Pred. No. 2.3e-101;
0; Mismatches 167;
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1 (bases 1 to 686)

Buell, C.R., Hart, A., Baker, B., Tanksley, S., Fry, W., Smart, C., Buelt, C.S., Griffiths, H., van der Hoeven, R., Tsai, J. and Karamycheva, S.A.

Karamycheva, S.A.

Generation of a set of potato cDNA clones for microarray analyses
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BQ508623.2 GI:21924395
EST
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686 bp mRNA linear EST 07-MAR-2003
EST616038 Generation of a set of potato cDNA clones for microarray
analyses mixed potato tissues Solanum tuberosum cDNA clone STMGX37
4
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on Jun 10, 2002 this sequence version
Other ESTS: EST616039
Contact: Robin Buell
                                                                                                                                                                                                                                                                                                                                                                   http://genome.arizona.edu/orders/
Seq primer: T3.
                                                                                                                                                                                                                                                                                                                                                                                               Email: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics
Institute. Orders can be made through URL:
                                                                                                                                                                                                                                                                                                                                                                                                                                             The Institute for Genomic Research 9712 Medical Center Dr, Rockville, MD
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GTTACAGAAACAGCTCTAGTCAACATGACCAGCATGGAATGTGGCCTTCCCCACCCTTTTG
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                                                       Conservative
                                                                                                                             /clone_lib="Generation of a set of potato cDNA clones for microarray analyses mixed potato tissues" /note="Vector: pBluescript SK(-); Site_1: EcoRI, Site_2: XhoI; supplier: Combination of untreated and Phytophthora infestans-treated libraries of stolons, leaves, leaflets, axillary buds of stem explants, petioles, germinating eyes, tubers, or roots."
                                                                                                                                                                                                                                                                                                           Tom/
                                                                                                                                                                                                                                 tissue_type="mixed tissues"
/lab_host="SOLR"
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/db_xref="taxon:4113"
                                                                                                                                                                                                                                                                clone="STMGX37"
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Solanum tuberosum
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                                                                     primer: M13F-R
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van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Bougri,O., Buell,C.R., Ronning,C., Tanksley,S. and Generations of ESTs from sprouting potato eyes Unpublished (2000)
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
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EST504916 cSTS Solanum tuberosum cDNA clone
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1 (bases 1 to 792)
                                                                                                                                                                     This clone can be obtained from the Univer Institute. Orders can be made through UKL: http://genome.arizona.edu/orders/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTGGTTGATGGGAACGCTGGACCTATAACTGGGGATGAGACGGTACCCTATCATTCACTC
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                                                                                                                                                                                                                                                              potato-array@tigr.org
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                  from the University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear EST 07-MAR-2003 e cSTS27C13 5' sequence,
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RESULT 10
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 SOURCE
ORGANISM
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VERSION
KEYWORDS
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                                                     CDNA 3', mRNA sequence.
CV478732
CV478732.1 GI:53703508
                                                                                                           CV478732 694 bp mRNA linear EST 01-OCT-200 Lu8B4 Flax fiber enriched Lambda ZapII Library Linum usitatissimum
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                                                                                                                                                                                                                                                                                                        CATTCCCAATATGACAAAGTTAGCTACAATGAAGTACATAACCTATTATGAGGATTCTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AATCCTCTGACTCCTTGGGAGAGACACCTATAAAAAATGTATTTTGCATATATGGTGCT 1227
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/clone="STS27C13"
/tlssue_type="sprouting eyes from tubers"
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/dev_stage="12-14 weeks post harvest"
/lab_host="SOLR"
/clone_lib="cSTS"
/clone_lib="cSTS"
/clone_lib="cSTS"
/clone_tyector: pBluescript SK(-); Site_1: EcoRI; Site_2:
/note=""vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
/note=""vector: pBluescript SK(-); The corner to the sizes of sprouting eyes (2mm to 15mm) were
taken from tubers. The tubers were incubated at 26C in the
dark for 2-3 weeks prior to sprouting. The eyes were
frozen in liquid nitrogen immediately upon removal from
tubers."
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74.2%;
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Pred. No. 1.9e-98;
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Matches 443;
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1 (bases 1 to 694)

2 (bay, A., Addi, M., Kim, W., David, H., Bert, F., Mesnage, P., Rolando, C. Chabberts B., Neutelings, G. and Hawkins, S. N.

2 (bases 1 to 694)

3 (bases 1 to 694)

4 (bases 1 to 694)

4 (bases 1 to 694)

5 (bases 1 to 694)

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6 (bases 1 to 694)

7 (bases 1 to 694)

8 (bases 1 to 694)

9 (bases 1 to 694)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCCTTTTGTCTTTTCACAGCCCGTGAACTAGCAGATGGGACTCTTTTCAAAGCAATAGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATGGTGCTCATATAGACAGAGGTTGGTTATTACTTTGCCCCAAGTGGCAAACCTTATC
AGCCAGAACACGATGGAAGCGACGTACATGTGGAACTAAATGTTGATCATGAGCATGGGT 1519
                                                                                             ATTCCTTATCTCTATGCAAGAGTTGGCTTGGACCAAAAGTCAACATAACACGGGCTCCCC
                                                                                                                                                                                                                                                                                                   CTGGGAATCTAGTGGAAGGGAATCCAGGAGCTACAAGTGGGGATGAGACGGTACCATACA
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primer: T3.
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/tbsue_type="Outer fiber-bearing tissues"
/tlsue_type="Outer fiber-bearing tissues"
/dev stage="Mid-flowering stage"
/dev stage="Mid-flowering stage"
/clone_lib="Flax fiber enriched Lambda ZapII Library"
/clone_lib="Flax fiber enriched Lambda ZapII Library"
/note="Site_1: XhoI; Site_2: EcoRI; mRNA were extracted
from field grown plants (Dunkerque, France). Following
harvest, roots, leaves and flowers were cut-off and
discarded, as were the bottom 10 cm of the stem. The
following bottom 15-cm section of the stem was then
isolated and the outer fiber-bearing tissues peeled off
and immediately frozen in liquid nitrogen. Library was
constructed using ZAP-cDNA synthesis kit and ZAP-cDNA
Gigapack III cloning kit (Stratagene)."
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/mol_type="mRNA"
/cultivar="Hermes"
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Pred. No. 5.5e-95;
0; Mismatches 147;
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AUTHORS
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BQ584361
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Best Local S
Matches 427
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Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes plant J. 32 (5), 845-857 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

1 (Dases 1 to 565)

Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski, M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA clone 024-003-K20 :
BQ584361
BQ584361.1 GI:26113938
EST
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                           CAAGGCCTGATAGTGGACTCTCTGCAATAACAGAACTTGACCCAGGTTACATAACAGGTC
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length: 565 Std Error: 0.00
length: K column: 20
3 row: K column: 20
imer: SP6; CATACGATTTAGGTGACACTATAG.
                                                                                                                                                                                                                 SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"
                                                                                                                                                                                                                                                                                                                                             /clone_lib="MPIZ-ADIS-024-inflorescence"
/note="Vector: pcMVSPOR76; Site 1: Sali; Site 2: NotI;
/note="Vector: pcMVSPOR76; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                                                                                                                                                                                                                                                                                                                                  orientation:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="inflorescence"
/lab_host="EMDH10B"
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/clone="024-003-K20"
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/mol_type="mRNA"
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                                                                                                                                21.4%;
                                                                                                       Score 350.8; DB 5;
Pred. No. 1.2e-93;
0; Mismatches 127;
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                                                                                                                     PCK FARMARD: T3 20mer
FORWARD: T3 20mer (backward)
BACKWARD: T7 21mer (backward)
FORWARD: T0W: C column:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CD710878 560 bp mRNA linear EST 25-JUN-2003 VVA026CO2 402285 An expressed sequence tag database for abiotic stressed leaves of Vitis vinifera var. Chardonnay Vitis vinifera
                                                                                                                                                                                                                                                                                                                                                    Unpublished (2002)
Contact: Cushman JC
                                                                                                                                                                                                                                                                                                                                                                                     Cramer,G.R. and Cushman,J.C.
An expressed sequence tag database
Vitis vinifera var. Chardonnay
                                                                                 Plate: 026 row: C column: 02
Seq primer: T7 20mer (forward)
High quality sequence stop: 560.
                                                                                                                                                                                                                                        MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Vitaceae; Vitis.
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Vitis vinifera
                                                                                                                                                                                                                                                                                                       Department of Biochemistry University of Nevada
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                                                                                                                                                                                                 PCR PRimers
                                                                                                                                                                                                                      Email: jcushman@unr.edu
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/organism="Vitis vinifera"
/mol_type="mRNA"
                                                               Location/Qualifiers
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                                              Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopaida; Poalea; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinaru
                                                                                                                                                 5', mRNA sequence.
CA090564
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SCSGAM2105C04.g AM2
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/clone="VVA026C02"
/tisme="ppe="leaf"
/tisme_type="leaf"
/dev_stäge="juvenile and adult"
/clone_lib="An expressed sequence tag database for abiotic stressed leaves of Vitis vinifera var. Chardomay"
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1:
ECoRI; Site_2: Xhol; Library construction was performed according to Stratagene's recommended protocol for the Lambda UniZapXR vector and cDNA synthesis kit."
676)
da Silva,F.R.,
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Contact: Arruda P
Centro de Biología Molecular e Engenharia C
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP,
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
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Plate: 105 row: C column: 04
Seq primer: T7 Promoter Primer.
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Clone distribution: clone distribution
through the Brazilian Clone Collection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The libraries that made SUCEST Genet. Mol. Biol. 24 (1-4), 1-7
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CGGCCCTTCTATAGTATTTTGCCCATTCAATGGGTAATAATGTCTTCAGATACTTTCTGGA
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/clone lib="AM2"
/clone lib="AM2"
/note="Organ: Apical meristem and tissues surrounding of immature plants; Vector: pSportl; Site 1: Sall; Site 2: Notl; An unidirectional cDNA library generated from [Apical meristem and tissues surrounding of immature plants]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"
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/db_xref="taxon:4547"
/clone="SCSGAM2105C04"
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Other name: 07-B-7; date: 6/30/99; Submitted to the Database of
Expressed Sequence Tags (dbEST) on 08/25/99; More information is
available at 'http://chrysie.tamu.edu/medicago'.
Seq primer: SKmod (CTA gAA CTA gTg gAT CC).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Department of Plant Biology
University of Minnesota
220 BioSci Center, 1445 Gortner
Tel: 612 624 2755
Fax: 612 625 1738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ESTs from uninoculated roots Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VandenBosch,K., Hur,J., Moore,J., Beremand,P., Peng,H. and Ellis,L. ESTs from uninoculated roots of Medicago truncatula (199b)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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EST.
Medicago truncatula (barrel medic)
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534 bp mRNA linear EST 26-
T110293e KVO Medicago truncatula cDNA clone pKVO-1E14, mRNA
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                         CAGATAGCAAGAGGGATGTTACACCAGTTAAAGAAGTTGTATCATGATGACCCTGTTTTTA 1168
                                                                                               CTTTCACAGCCCGTGAACTAGCAGATGGGACTCTTTTCAAAGCAATAGAAGACTATGACC 1108
                                                                                                                                                                          TTACAGAAACAGCTCTAGTCAACATGACCAGCATGGAATGTGGCCTTCCCACCCTTTTGT
                                                                                                                                                 ATGCTTGAAACTGGAAAATGCCC 676
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                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                              /clone lib="KV0"
/clone lib="KV0"
/note="Vector: pBluescript SK -; Site 1: EcoRI; Site 2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Medicago truncatula"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cultivar="genotype A17"
/db_xref="taxon:3880"
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                                                                                                                                                                                                                                          19.3%;
                                                                                                                                                                                                                      Score 316.4; DB 1;
Pred. No. 2.7e-83;
0; Mismatches 121;
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Korth,K., Scott,A.D., Harris,A.R., Gonzales,R.A. Flores,H.R., Inman,J.T., Weller,J.W. and May,G.I. Expressed Sequence Tags from the Samuel Roberts Medicago truncatula insect herbivory library Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NF097C07IN1F1054 Insect herbivory Medicago truncatula NF097C07IN 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Korth K
Dept. of Plant Pathology
University of Arkansas
217 Plant Science Building,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Medicago truncatula (barrel medic)
Medicago truncatula
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                                                                                                                                                                                                                                                                                                                                                 Email: kkorth@comp.uark.edu
Insert Length: 628 Std Error: 0.0
Plate: 097 row: C column: 07
Seq primer: TCACACAGGAAACAGCTATGAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 501 575 5191 Fax: 501 575 7601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BI267124.1 GI:14871872
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                                                                 /tissue_type="local and systemic leaves"
/dev stage="mature"
/dev stage="mature"
/clome lib="Insect herbivory"
/note="Vector: Lambda Zap; Library was produced from fully expanded M. truncatula leaves of plants fed upon by Spodoptera exigua (beet armyworm) for 24 hours. Systemic (undamaged leaves from injured plants) and wounded leaves were harvested and pooled."
                                                                                                                                                                                                                                                   /organism="Medicago truncatula"
/mol_type="mRNA"
/db_xref="taxon:3880"
                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                 clone="NF097C07IN"
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18.7%;
79.2%;
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                  DB 4;
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Query Match Best Local Similarity

Score 306.6; DB 4 Pred. No. 2.6e-80;

Length 628;

OY  108 CGACTACTCGAAGCTATCGGGTATAATCATTCCGGGATTTGCGTCGACGAGCTACGAGC
149 CGATTACTCTAAACTCTCCGGCATTATTATCCCAGGCTTCCATCCA
168 GTGGTCGATCCTTGACTGTCCATACACTCCGTTGGACTTCAATCCGCTCGACCTCGTATG
209 afdeft data this data this control of the contr
228 GCTAGACACCACTAAGCTTCTTCTGCTGTCAACTGCTGGTTAAGTGTATGGTGCTAGA
269 GCTCGACCACAAACTTCTTTCTGCTGAATTGTTTGGCTTAAGTGCACTGTTCTTGTGGAACTTCTTCTGCTTAAGTGCATGTTCTTTCT
288 TCCTTATAATCAAACAGACCATCCCGAGTGTAAGTCACGGCCTGACAGTGGTCTTTCAGC
329 CCCTTACAATCAAACAGATCATCCTGATTGTAAATCCCGTCCTGATAGCGGTCTTTCCGG 348 CATCACAGAATTGGATCCCAGGTTACATAACAGGTCCTCTTTCTACTGTCTGGAAAGAGTG
348 CATCACAGAATTGGATCCAGGTTACATAACAGGTCCTCTTTCTACTGTCTGGAAAGAGTG
Db 389 AATTACAGAGCTTGATCCAGGTTATATAACAGGACCTCTTTCGTCTGTATGGAAAGAATG 448
QY 408 GCTTAAGTGGTGTTTGAGTTTTGGTATAGAAGCAAATGCAATTGTCGCTGTTCCATACGA 467
Db 449 GATTAAGTGGTGTATTGAATTTGGCATANAAGCTAATGCAATAATTGCTGTTCCTTATGA 508
QY 468 TIGGAGATIGICACCAACCAAATIGGAAGAGCGIGACCITTACITICACAAGCICAAGTI 527
Db 509 TTGGAGACTGTCACCATCCATGCTTGAAGAACGAGACCTTTACTTTCATAAGCTTAAATT 568
Qy 528 GACCTTTGAAACTGCTTTAAAACTCCGTGGCGGCCCTTCTATAGTATTTGCC 579
Db 569 GACATTTGAGACTGCTTT-CAACTTCGAGGNGGCCCCTCTTTANTTTTTGGC 619
Search completed: November 9, 2005, 08:31:22

Search completed: November 9, 2005, 08:31:2: Job time : 5649 secs